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January 21, 2003, 23:02:20 ; Search time 775.333 Seconds (without alignments) 1576.506 Million cell updates/sec
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GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
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Listing first 45 summaries
                                         OM nucleic - nucleic search, using sw model
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Pred. No. is the number of results predicted by chance to have a

PRI 21-AUG-1997

HSPPARGAM 1766 bp mRNA linear PRI 21-AUG. H.sapiens mRNA for peroxisome proliferactor activated receptor gamma.

HSPPARGAM LOCUS DEFINITION

RESULT 1

ALIGNMENTS

Dukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi, Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
1 (bases 1 to 1766)
Lambe, K.G. and Tugwood, J.D.
A human peroxisome-proliferator-activated receptor-gamma is

peroxisome proliferator-activated receptor gamma. Homo sapiens Homo sapiens

VERSION KEYWORDS SOURCE ORGANISM

REFERENCE AUTHORS TITLE

X90563 X90563.1 GI:1480099

ACCESSION

AX409565 Sequence
AX120042 Homo sapien
AX151002 Sequence
AX120042 Homo sapi
AX095174 Homo sapi
AX093174 Homo sapi
AX093174 Homo sapi
AX093174 Homo sapi
AX093178 Homo sapi
AX09318 Rattus no
U63415 Human perox
AX09318 Rattus no
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U63415 Human perox
AX12467 Sequence
D81231 Homo sapien
AX203332 Sequence
D81231 Homo sapien
AX120485 Rattus no
AX120485 Rattus no
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AX11044 Mus muscu
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AX11341 Mus muscu
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AX1419 Synthetic
AX06176 Homo sapi
AX07869 Macaca fa
AX071819 Synthetic
AX06176 Homo sapi
AX155512 Human DNA
AX1619 Synthetic
AX06176 Homo sapi
AX155812 Human DNA
AX1619 Synthetic
AX1619 Synthetic
AX06176 Homo sapi
AX155812 Human DNA
AX1618 AX1618 Synthetic
AX1618 AX16 score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution. SUMMARIES HSPPARGAM HUMPPARGB AX409565 AX139020 AC120042 AX151002 AX00552181 AC093174 AC027126 AL450321 AY071819 AC114359 HSU63415 AR121467 AL139090 AC120485 BTPPARG1 AC111044 AC084108 AC113481 AR203332 HUMPPARG AC084401 AC121723 RN75P15 AY048699 AL135778 HUMPAXBA AC090947 HSU79012 AY048697 AC102093 12 10 DB 71.9 1766 71.9 1808 71.9 1808 59.5 170940 57.1 18667 57.1 18667 57.1 18667 57.1 18667 57.1 18667 57.1 18667 57.1 18667 57.1 18667 57.1 18667 57.1 18668 54.8 1679 54.8 1679 54.8 1679 54.8 1679 54.8 1679 54.8 1679 54.8 1679 54.8 1679 54.8 1679 54.8 1679 54.8 1679 55.2 194914 56.2 194914 57.3 192770 57.3 Query Match Length Score 
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4 (bases 1 to 1808)
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                                                                                                                 Lambe, K.G.
Direct Submission
Direct Submission
Submitted (07-AUG-1995) K.G. Lambe, Zeneca Central Toxicology Lab.,
Alderley Park, Macclesfield, Cheshire SKIO 4TJ, UK
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /db_xref="G1:1490314"
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GDRPGLLNVKPIEDIQDNLLQALELQUKLNHPESSQLFAKLLQKYTDLRQIVTEHVQL
LQVIKKTETDMSLHPLLQEIYKDLY"
414 c 397 g 425 t
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Homo sapiens peroxisome proliferator activated receptor gamma
(PPARG) mRNA, complete cds.
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SNSLMAIECRVGGDKASGFHYGVHACEGCKGFFRRTIRLKLIYDRCDLNCRIHKKSRN
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activated by inducers of adipogenesis, including thiazolidinedione
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Best Local Similarity 91.4%; Pred. No. 0.31;
Matches 32; Conservative 0; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                            'note="alternative start site"
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Chases 1 to 1808)
Qi.J.S., Desai-Yajnik,V., Greene,M.E., Raaka,B.M., and Samuels,H.H.
The ligand-binding domains of the thyroid hormone/retinoid receptor gene subfamily function in vivo to mediate heterodimerization, genrallencing, and transactivation
Mol. Cell. Biol. 15 (3), 1817-1825 (1995)
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SNSLMAIECRVCGDKASGFHYGVHACEGCKGFFRRTIRLKLIYDRCDLNCRIHKKSRN
                                                         (Dassel 1 to 1808)

Greene, W.E., Blumberg, B., McBride, O.W., Yi, H.F., Kronquist, K., Kwan, K., Hsieh, L., Greene, G. and Nimer, S.D.

Isolation of the human peroxisome proliferator activated receptor gamma cDNA: expression in hematopoietic cells and chromosomal
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo
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Kwan, K., Hsieh, L., Greene, G. and Nimer, S.D.
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On Dec 26, 2001 this sequence version replaced gi:722619.
Location/Qualifiers
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Best Local Similarity 91.4%; Pred. No. 0.31;
Matches 32; Conservative 0; Mismatches 3;
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Gene Expr. 4 (4-5), 281-299 (1995)
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73. .1606
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/db_xref="taxon:9606"
/chromosome="3"
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1. .1808
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"Berreng Berrang N. Bastien V., Lander, E., Ali, A., Allen, N., Anderson, S., Barrang N., Bastien V., Bloom, T., Boguslavkiy, L. Anderson, S., Barrang, N., Bastien V., Bloom, T., Boguslavkiy, L., Anderson, S., Barrang, N., Bastien V., Bloom, T., Boguslavkiy, L., Anderson, S., Chorpell, Y., Colangelo, M., Collins, S., Collymore, A., Chargo, B., Gorde, P., Cooke, P., Deakellano, K., Domes, J. S., Dodge, S., Paro, S., Gertela, P., Filthug, M., M., Collins, S., Collymore, A., Grand, J., Grand, P., Halle, M., Tiley, J., Ohnson, K., Jonson, K., Jonson, R., Jonson, C., Machen, E., Horton, L., Hilme, W., Hilso, J., Ohnson, K., Liu, G., Machen, C., Machen, P., McKernan, K., Mardhad-Toh, K., Liu, G., Machen, C., Machen, P., McKernan, K., Mardhad-Toh, Micol, R., Micol, R., Mischer, C., Machen, P., McKernan, K., Maldrim, J., Meneus, L., Mihova, T., Margad, V., Wubpy, T., Naylor, J., Marquis, N., Matthews, C., Machen, C., North, C., Oromor, T., O'Donnell, P., O'Neil, D., O'Iver, J., Peterson, P., Barnca, R., Schauer, S., Schupback, R., Straus, C., Rayman, C., Barnca, R., Schauer, S., Schupback, R., Straus, C., Rayman, J., Zehne, R., Stange, P., Milson, B., Mux, M., Mardhan, M., Tarid, M., Nicol, North, C., Marchan, A., Talamas, J., Vassiliev, H., Viell R., Wall, M., Martie, M., Milson, B., Mu, X., Myman, D., Ye, M.J., Young, G., Stanger, L., Martie, M., Martie, M., Martie, M., Martie, M., Martie, M., Charace, L., Cander, M., Cangolo, M., Collins, S., Collymore, A., Charace, L., Camporland, M., Sage, D., Grazzo, B., Chopel, Y., Colangelo, M., Collins, S., Collymore, A., Canazo, B., Chopel, Y., Colangelo, M., Collins, S., Collymore, M., Cander, D., Martie, M., 
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                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                        1 (bases 1 to 170940)
Birran, B., Nusbaum, C. and Lander, E.
Homo sapiens chromosome 8, clone RP11-659E9
Unpublished
                                                        Homo sapiens
                                                        ORGANISM
                                                                                                                                                                                                                       JOURNAL
REFERENCE
AUTHORS
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                                                                                                                                                                 PAT 14-JUN-2002
                                                                                                                                                                                                                                                                                                                                                          Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Patent: US 6200802-A 1 13-MAR-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 30.2; DB 6; Length 1811;
Pred. No. 0.31;
0; Mismatches 3; Indels 0;
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Patent: WO 0229103-A 2212 11-APR-2002;
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157 CGCCGTGGCCGCAGAATGACCATGATTGACACAG 191
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                                                                                                                                                   Sequence 2212 from Patent W00229103. AX409565
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Sequence 1 from patent US 6200802.
AR139020
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/db_xref="taxon:9606"
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1 (bases 1 to 1844)
Greene, M.E. and Blumberg, B.
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SE Birren, B. Nusbaum, C. Lander, E., Ali, A., Allen, N., Anderson, S., Barna, N., Bastien, V., Bloom, T., Boguslavkiy, L., Boukhgalter, B., Comarata, J., Chang, J., Chazaro, B., Choepel, Y., Collymore, A., Cooke, P., DeArellanc, K., Dewar, K., Diaz, J.S., Dodge, S., Farco, S., Ferreira, P., FitGerald, M., Gage, D., Galagan, J., Gardon, S., Gord, S., Graham, L., Grand-Pierre, N., Hagos, B., Horton, L., Hulme, W., Illev, T., Johnson, R., Jones, C., Kamat, A., Karatas, A., Kells, C., Landers, T., Levine, R., Lindblad-Toh, K., Liu, G., MacLean, C., Macdonald, P., Major, J., Matthews, C., McCarthy, M., Neldin, J., Meneus, L., Milova, Y., Pterson, K., Phunkhang, P., Pierre, N., Raymond, C., Nacol, R., Norbu, C., Norman, C., O'Connor, T., O'Donnell, P., O'Neil, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Raymond, C., Retta, R., Rise, C., Royar, P., Smith, C., Spencer, B., Stange-Thomann, N., Scojanovic, N., Talamas, J., Verell, R., Vo, A., Wilson, B., Wu, X., Myman, D., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.
O'Connor,T., O'Donnell,P., O'Neil,D., Oliver,J., Peterson,K., Phukhang,P., Pierre,M., Raymond,C., Retta,R., Rise,C., Rogov,P., Roman,J., Roy,A., Schauer,S., Schubback,K., Semann,S., Severy,P., Smith,C., Spencer,B., Stange-Thomann,N., Stojanovic,N., Talamas,J., Tesfaye,S., Theodore,J., Topham,K., Travers,M., Vassiliev,H., Viel,R., Vo'A., Wilson,B., Wu,X., Wyman,D., Young,G., Zainoun,J., Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (06-AUG-2002) Whitehead Institute/MIT Center for Genome Research, 32 Charles Street, Cambridge, MA 02141, USA ON Aug 2, 2002 this sequence version replaced gi:21327565. All repeats were identified using RepeatMasker:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Center: Whitehead Institute/ MIT Center for Genome Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: sequence submissions@genome.wi.mit.edu
------ Project Information
Center project name: L26752
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /clone="RP11-659E9"
/clone_lib="RPCI-11 Human Male BAC"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Web site: http://www-seg.wi.mit.edu
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/db_xref="taxon:9606"
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/map="8"
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/rpt_family="L1MCa"
5019. 6402
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complement (6888. .7343)
/rpt_family="L1M4"
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/rpt_family="(CAA)n"
4187. .4887
/rpt_family="LiPBI"
4888. .4940
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4157. .4186
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PAT 22-JUN-2001
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synthetic construct
artificial sequences.
1 (bases 1 to 33)
Nomose,Y., Maekawa,T., Odaka,H. and Kimura,H.
5-membered n-heterocyclic compounds with hypogylcemic and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 9; Length 170940;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                family="MER114"
7. 15877
                                                                                                                                             complement(10754. .10847)
/rpt_family="MIR"
complement(10908. .11214)
                                                                                                                                                                                                                             /rpt_family="A-rich"
complement(13443, .13496)
/rpt_family="MER94"
                                                                                                                                                                                                                                                                                                                                             rpt_family="AluJb"
449I. 1455
                                                                                                                                                                                                                                                                                                                                                                                                             family="AluSx"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  complement(17438. .17591)
'rpt family="MIR"
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Sequence 1 from Patent WO0138325.
AX151002
                                                             /rpt_family="Charlie2"
complement(8163..8442)
/rpt_family="Charlie2"
/rpt_family="Charlie2"
complement(7734. .7963)
/rpt_family="L2"
                                             complement (7993. .8117)
                                                                                                                                                                                                                                                                                                                                                                                               /rpt_family="(TTTTA)n"
complement(14536. .148
                                                                                                                                                                                                                                                                                                                                                                                                                                              14899. .14927
/rpt_family="AT_rich"
complement(15498. .158
                                                                                                                                                                                                                                                                                                                               /rpt_family="AT_rich"
complement(14162...14.
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                                                                                                                             family="MLT1G1"
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23601. .23633
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   family="LIMC1"
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4096...14100
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10205.
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Homo sapiens.
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                                                                                                            SOURCE
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (03-JUJ-1997) Hideki Okazawa, Kobe University School of Medicine, 2nd Department of Internal Medicine, 7-5-1 Kusunoki-chocho-ku, Kobe 650, Japan (E-mail:okazawa@med.kobe-u.ac.jp,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Okazawa,H., Mori,H., Tamori,Y., Araki,S., Niki,T., Masugi,J., Kawanishi,M., Kubota,T., Sinoda,H. and Kasuga,M.
No coding murations are detected in the peroxisome proliferator activated receptor gene in Japanese patients with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /product="peroxisome proliferator activated-receptor
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                                                                                                                                                                                         DB 6; Length 33;
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Pred. No. 86;
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                                                                                  /organism="synthetic construct"
/db_xxref="taxon:32630"
/note="Primer for cloning PPAR? gene"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               'note="ppar gamma common exonl"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Tel:81-78-341-7451, Fax:81-78-382-2080)
Location/Qualifiers
hypolipidemic activity
Patent: WO 0138325-A 1 31-MAY-2001;
Takeda Chemical Industries, Ltd. (JP)
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100.0%; Pred. No. ...
... 0; Mismatches
                                                                                                                                                                                  58.6%; Score 24.6; I 87.1%; Pred. No. 54;
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                                                                                                                                                                                                                                                     12 GTGGTGGCAGAATGACCATGGTTGACACAG 42
                                                                                                                                                                                                                                                                             organism="Homo sapiens"
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/tissue_type="placenta"
<115. .340
/gene="ppar gamma"
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Diabetes (1997) In press
2 (bases 1 to 416)
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                                                                                                                                                                                                     Similarity 87.1%;
27; Conservative
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RESULT 8 AC093174

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1 (bases 1 to 13567)

Bao,J., Bao,O., Bao,W., Bian,X., Cao,T., Chen,C., Chen,J., Ding,H., Dong,W., Fan,H., Peng,X., Gong,J., Guan,Q., Gu,X., Guo,D., Guo,Z., Li,G., Hu,J., Li,L., Liu,Y., Kang,N., Li,C., Li,C., Li,F.,

Li,W., Li,W., Li,Y., Luo,J., Niu,Y., Tau,Y., Liu,N., Liu,B., Liu,Y., Song,L., Song,S., Sun,M., Sun,R., Wang,Y., Tan,X., Tao,X., Song,L., Song,J., Wang,J., Wang,J., Wang,J., Wang,J., Wang,J., Wang,J., Wang,X., Wang,X., Wang,X., Wang,X., Wang,X., Wang,X., Zhang,X., Zhang,X., Zhang,X., Zhang,X., Zhang,X., Zhang,X., Zhang,Y., 
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Unpublished
Chases I to 13567)

S Gases I to 13567)

Bao, J., Bao, W., Blan, X., Cao, T., Chen, C., Chen, J., Ding, H., Dong, W., Fan, H., Feng, X., Gong, J., Guan, Q., Gu, X., Guo, D., Guo, Z., He, L., Hu, S., Huang, F., Jin, Y., Kang, N., Li, C., Li, C., Li, F., Li, S., Li, T., Li, Li, Y., Liu, B., Liu, B., Liu, B., Liu, W., Li, W., Li, W., Li, W., Li, W., Li, W., Li, W., C., Li, F., Li, W., Li, W., Li, W., Li, W., Li, W., Li, W., C., Song, L., Wang, L., Wang, L., Wang, L., Wang, L., Wang, K., Wang, X., Wang, X., Wang, Y., Wu, D., Wu, Q., Xie, F., Xuan, Z., Xue, Y., Yan, C., Yang, X., Yu, B., Zhang, X., Zhan
                                          PRI 13-AUG-2001
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Submittad (13-AUG-2001) Human Genomic Center, Institute of
Genetics, Chinese Academy of Sciences, Datun Road, Beijing, Beijing
100101, P.R.China
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Insert size: 1198; sum-of-contigs
Onality coverage: 1.48x in Q20 bases;sum-of-contigs
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Sequencing vector: pUC18; 100% of reads
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Assembly program: Phrap, version 0.990329
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S Wu,O., Bao,J., Bao,Q., Bao,W., Bian,X., Cao,T., Chen,C., Chen,J., Ding,H., Dong,W., Fan,H., Feng,X., GaongJ., Guan,Q., Gu,X., Guo,D., Guo,Z., He,L., Hu,S., Hang,F., Jin,Y., Kang,N., Li,C., Li,C., Li,C., Li,C., Li,C., Li,T., Li,Y., Liu,Y., Liu,N., Liu,B., Liu,Y., Liu,Y., Liu,Y., Liu,N., Liu,B., Liu,Y., Liu,Y., Liu,Y., Liu,N., Liu,B., Liu,Y., Liu,Y., Liu,Y., Liu,N., Liu,B., Song,J., Song,S., Sun,M., Sun,W., Sun,Y., Tao,R., Wang,H., Wang,J., Wang,J., Wang,J., Wang,J., Wang,J., Wang,J., Wang,J., Wang,X., Wang,X., Wang,X., Yan,C., Yang,X., Yan,C., Yang,X., Zhang,X., Zhang,H., Zhang,H., Zhang,H., Zhang,M., Zhang,Y., Zhang,X., Zhang,Y., Z
                                                                                                                                                                                                                                                                                                                                                                  AC090947 166043 bp DNA linear PRI 20-MAR-2001 Homo sapiens chromosome 3 clone RPI1-30G23 map 3p, complete
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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http://www.genomics.org.cn
                                                                             Db 109924 CAGAAATGACCATGGTTGACACAG 109947
19 CAGAAATGACCATGGTTGACACAG 42
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AC090947.1 GI:13384351
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/organism="Homo sapiens" /db\_xref="taxon:9606"

Location/Qualifiers

source

FEATURES

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Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases I to 185608)

88 Wu,O., Bao,J., Bao,W., Bian,X., Cao,T., Chen,C., Chen,J., Ding,H., Dong,W., Fan,H., Feng,X., Gong,J., Gang,Q., Gu,X., Guo,D., Li,F., Li,G., Li,V., Li,T., Liu,Y., Liu,N., Liu,B., Li,F., Li,G., Li,C., Li,C., Li,C., Li,C., Li,C., Li,C., Li,Y., Li,W., Li,W., Li,W., Li,W., Li,Y., Luo,C., Luo,J., Nau,Y., Qi,O., Qi,X., Song,L., Song,S., Sun,M., Sun,W., Sun,Y., Tao,R., Wang,H., Wang,J., Wang,J., Wang,J., Wang,J., Wang,J., Wang,J., Wang,L., Yan,C., Zhang,Y., Zhu,B., 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (06-MAR-2001) Human Genomic Center, Institute of Genetics, Chinese Academy of Sciences, Datun Road, Beijing, Beijing
                                                                                                                                                                                                                                                                                                       ·.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRI 06-MAR-2001
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Tao,R., Hu,S., Dong,W., Wang,J., Yang,X., Cheng,C., Wang,Y., Niu,Y.
Qi,X., Li,T., Zhang,H., Liu,N., Wu,D., Yu,B., Fan,H., Liu,Y.,
Li,G., Li,C., Bao,Q., Bao,J., Wang,X., Song,L., Zhang,L., Guo,D.,
Huang,F., Zhang,G., Li,J., Bian,X., Zhang,M., Li,L., Feng,X., Yu,J.
                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AC027126 185608 bp DNA linear PRI 06-W40mo sapiens chromosome 3 clone RP11-586C12 map 3p, complete
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0
                                                                                                                                                                                                         Length 166043;
                                                                                                                                                                                                                                                                                                   0; Indels
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                               /clone="RP11-30G23"
48570 a 35113 c 34446 g 47914 t
                                                                                                                                                                                                         ch 57.1%; Score 24; DB 9
1 Similarity 100.0%; Pred. No. 71;
24; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Db 117076 CAGAAATGACCATGGTTGACACAG 117053
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          --Genome Center
                                                                                                                                                                                                                                                                                                                                                                               19 CAGAAATGACCATGGTTGACACAG 42
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Center code:Beijing
/map="3p"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens.
                                                                                                                                                                                                     Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                and Yang, H.
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Center: UK Medical Research Council
                                                                                                                                                                                                                                                1. .209175
/organism="Mus musculus"
/db_xref="taxon:10090"
                                                                                                                                                                                                                                                                                                                                /chromosome="13"
/clone="RP23-232M10"
                                                      Genome Center
                                                                                                                                                                                                                         Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AC099350.4 GI:21717844
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       73.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   55.7%;
                                                                                                            Center code: UK-MRC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 73.2
Matches 30; Conservative
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  For further detai
VECTOR: pBACe3.6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Norway rat
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ORIGIN
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KEYWORDS
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                                                                                                                                                                                                                         FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AL450321 209175 bp DNA linear ROD 29-JUN-2002 Mouse DNA sequence from clone RP23-232M10 on chromosome 13,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.

This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest. The following
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em:, EMBL; Sw:: SWISSPROT; Tr:, TREMBL; Wp:, WORMPEP; Information on the WORMPEP database can be found at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ·.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (19-UNN-2002) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CE10 15A, UK. E-mail enquiries:
hunquery@sanger.ac.uk clone requests: clonerequest@sanger.ac.uk
on Un 15, 2001 this sequence version replaced gi:14330010.
During sequence assembly data is compared from overlapping clones.
Where differences are found these are annotated as variations
together with a note of the overlapping clone name. Note that the
variation annotation may not be found in the sequence submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 209175)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          http://www.sanger.ac.uk/Projects/C elegans/wormpep RP23-232M10 is
from the RPCI-23 Mouse PAC Library
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 57.1%; Score 24; DB 9; i ngth 185608; Best Local Similarity 100.0%; Pred. No. 71; Matches 24; Conservative 0; Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                                                                                             Insert size: 185608; sum-of-contigs
Quality coverage: 10.96x in Q20 bases;sum-of-contigs
                                                                                                                             Sequencing vector: pUC18; 100% of reads
Chemistry: Dye-terminator: FT 55% of reads
Achemistry: Dye-terminator Big Dye; 45% of reads
Assembly program: Phrap; version 0.990329
Consensus quality: 18758 bases at least Q40
Consensus quality: 18956 bases at least Q30
Consensus quality: 18956 bases at least Q30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       53641 a 40367 c 39222 g 52378 t
                            Project Information
                                                                                                         ----- Summary Statistics
                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="3"
                                                                          Center clone name: RP11-586C12
                                                   Center project name:1% project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Db 161293 CAGAAATGACCATGGTTGACACAG 161270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /clone="RP11-586C12"
                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
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Contact:hgc@igtp.ac.cn
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ORIGIN
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AL450321/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DEFINITION
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VERSION
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TITLE
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Muzny, D.M., Adams, C. & Adio-Oduola, B., Ali-osman, F.R., Allen, C., Alsbrooks, S.L., Amaratunge, H.C., Are, J.R., Ayele, M., Banks, T., Babrooks, S.L., Benton, J., Bimage, K., Blankenburg, K., Bannin, D., Bouck, J., Brieda, W., Brown, E., Brown, M., Bryant, N.C., Carron, E., Burch, P., Burkett, C., Burnell, K.L., Byrant, N.C., Carron, T.R., Carter, M., Cavazos, S.R., Chacko, J., Chavez, D., Chen, G., Chen, R., Chen, Z., Chowdhy, I., Chardon, J., Chard, N.C., Chen, R., Chen, T., Chen, Z., Chowdhy, I., Chardon, J., Chard, N.C., Chen, R., Chen, Z., Chowdhy, I., Chardon, J., Carter, M., Cavazos, S.R., David, R., Dargar, D., Edward, C., Davy, Carroll, L., Ding, Y., Dinh, H.H., Douthwaite, K. J., Darger, H., Dugan-Rocha, S., Durbin, K.J., Barnharte, F., Ragar, D., Edwards, C.C., Elhaj, C., Escotto, M., Falls, T., Serraguto, D., Flagg, N., Ford, J., Ford, J., Garza, N., Gill, R., Gorrell, J.H., Guevaza, M., Ganrarne, P., Hales, S., Hanilton, K., Harris, C., Harris, K., Hart, M., Havlak, H., Holloway, C., Hollins, B., Hernandez, O., Hodgson, A., Houles, M., Holloway, C., Hollins, B., Jan, Y., Johnson, R., Holler, S., Hume, J., Jackson, L., Katlovic, J., Kureshi, A., Landry, N., Lea, B., Lewis, L.C., Lewis, L., Li, J., Li, J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HTG 11-JUL-2002
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Rattus norvegicus clone CH230-6013, *** SEQUENCING IN PROGRESS ***,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Gaps
constructed by the group of Pieter de Jong. For further details see http://www.chori.org/bacpac/home.htm
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 209175;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         11; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 23.4; DB 10;
Pred. No. 1.2e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 GACCTACCCCGTGGTGGCAGAATGACCATGGTTGACACAG 42
                                                                                                                                                                                                                                                                                                          Web site: http://mrcseq.har.mrc.ac.uk
Contact: mouseq@har.mrc.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Mismatches
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56180 a 44574 c 46218 g 62203 t
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contig of 2259 bp in length gap of unknown length contig of 4449 bp in length gap of unknown length length gap of unknown length length gap of unknown length 
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g of 7783 bp in length
f unknown length
f unknown length
f unknown length
g of 6899 bp in length
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bp in length
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bp in length
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of 5807 bp in length
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of 6633 bp in length
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                                                                                                                                                                                                                                                                                                                                                                                                        contig of 1241 by gap of unknown lagant of unknown lagant of unknown lagant of 1266 by gap of unknown lagant of 1255 by gap of unknown lagant of unknown lag
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gap of unknown le
contig of 1530 by
gap of unknown le
contig of 1702 by
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           Sodergren, E., Sonaike, T., Sparks, A., Stanley, H., Stone, H., Sutton, A., Svatek, A., Tabor, P., Tamerisa, A., Tamerisa, K., Tang, H., Tansey, J., Taylor, C., Taylor, T., Telfrod, B., Thomas, N., Thomas, S., Usmani, K., Vasquez, L., Vera, V., Villalon, D., Vinson, R., Mang, O., Wang, S., Ward-Moore, S., Warren, R., Washington, C., Wallington, R., Williams, G., Williamson, A., Wleczyk, R., Wooden, S., Worley, K., Weitz, K., Woyden, S., Worley, K., Weitz, G. and Gibbs, R. Direct Submission Gibbs, R. Direct Submission Unpublished
                                                                                                                                                                                                                                                                                                                                                                              Submitted (10-NOV-2001) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA (asses 1 to 267260) Worley,K.C. Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (11-JUL-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA On Jul 10, 2002 this sequence version replaced gi:17941836.
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Scherer, S., Scott, G., Shen, H., Shooshtari, N., Sisson, I.,
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Sequencing vector: Plasmid;
Assembly program: Phrap; version 0.990329
Consensus quality; 21495 bases at least Q40
Consensus quality: 220002 bases at least Q20
Consensus quality: 220002 bases at least Q20
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Center code: BCM
Web site: http://www.hgsc.bcm.tmc.edu/
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13635: gap of unknown
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Direct Submission
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COMMENT

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On Dec 23, 1998 this sequence version replaced g1:4049327.
All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html.
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/rpt_family="MLT18"
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complement(9022, 9239)
/rpt_family="MERS8A"
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8643. .8726
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1308. .11591
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        10146. .10442
/rpt_family="LTR16C"
10847. .11158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .5513
family="AluYa5"
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1592. .11623
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /rpt_family="MLT1B"
complement(4591..48
                                                                                                                 Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                               /rpt_family="THE18"
2428. .3054
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1329. .4398
/rpt_family="(TA)n"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3370. .6435
'rpt_family="MADE1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   complement (7081, .7; /rpt_family="AluSg"
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.2254. .12273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           rpt_family="MER63"
060_ 3127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         'rpt_family="AluSg"
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complement(4287, .
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10146. .10442
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              rpt_family="L2"
1477. .3272
                                                                                                                                                                                                                       'chromosome="17"
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No. A., Wagner, A., Wheeler, J., Wu, X., Wyman, D., Ye, W.J. and Zody, M. Direct Submission

Research, 320 Charles Street, Cambridge, MA 02141, USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AC006080 191111 bp DNA linear PRI 23-DEC-1998
Homo sapiens chromosome 17, clone hRPR.394_K_10, complete sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
Eukaryota; Metazoa; Chordata; Cranlata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                             Score 23.4; DB 2; Length 267260;
Pred. No. 1.2e+02;
0; Mismatches 11; Indels 0;
contig of 8862 bp in length
gap of unknown length
contig of 8726 bp in length
gap of unknown length
contig of 10406 bp in length
contig of 10406 bp in length
contig of 11019 bp in length
contig of 11019 bp in length
grap of unknown length
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grap of unknown length
                                                                                                                                                                                                                 contig of 17079 bp in length
gap of unknown length
contig of 26150 bp in length
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Birren, B., Linton, L., Nusbaum, C. and Lander, E.
Homo sapiens chromosome 17, clone hRPK.394_K_10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Db 26039 AGACACCCCATTGGGGCGCACAACGGACAATGGGTGACACA 26079
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AC006:380.1 GI:4056515
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nilarity 73.2%;
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Best Local Similarity
Matches 30; Conserv
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163072
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MURLY, D.M., Adams, C., Adio-Oduola, B., Ali-osman, F.R., Allen, C., Alabaria, J., Banas, I. (Dassas I to 194914)

Barbaria, J., Benton, J., Bilmed, B., Blankenburg, K., Bonnin, D., Bouck, J., Bure, S., Blankenburg, K., Bonnin, D., Bouck, J., Burkenburg, R., Bonnin, D., Bouck, J., Burkenburg, R., Bonnin, D., Bouck, J., Burkenburg, R., Bonnin, D., Bonds, S., Erreva, M., Erwan, E., Brown, M., Bryant, N. P., Carcon, C., Chen, R., Chen, C., Chan, C., Coyle, M.D., Datborne, S.R., David, R., Carcid, D., Edwards, C.C., Edwards, C.C., Edwards, C.C., Edwards, C.C., Edwards, C.C., Edwards, C., David, R., Garrer, T., Garrer, P., Frantz, P., Farls, K., Hart, M., Hard, R., Harnandez, O., Hodgson, M., Garrer, T., Garrer, P., Harnandez, J., Hernandez, O., Hodgson, M., Hogues, M., Holloway, C., Hame, J., Jackson, L.E., Jacobson, B., Jai, Y., Johner, R., Holly, S., Hume, J., Jackson, L.E., Jacobson, B., Jai, Y., Johner, M., Hollyer, R., Martin, R., Mart
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AC114359 194914 bp DNA linear HTG 13-JUL-200 Rattus norvegicus clone CH230-72G23, *** SEQUENCING IN PROGRESS ***, 74 unordered pieces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Norway rat.
Rattus norvegicus
Eukaryota, Metazoa; Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae,
                                                                                                                                                                                                                                           Gaps
                                                                                                                                                               Query Match 55.2%; Score 23.2; DB 9; Length 191111; Best Local Similarity 77.8%; Pred. No. 1.4e+02; Matches 28; Conservative 0; Mismatches 8; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                Db 111225 ACATTTCCCCTGGAGGCAAATTGACCCTGGTTGAC 111190
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      .31521)
complement (31358. .31
/rpt_family="MLT1J"
32404. .32706
/rpt_family="AluSx"
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HTG; HTGS_PHASE1.
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Worley, K.C.
Direct Submission
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NOTE: This is a 'working draft' sequence. It currently consists of 74 contigs. The true order of the pieces is not known and their order in this sequence record is
Submitted (08-MAR-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA 3 (bases I to 194914) Worley, K.C.

Direct Submission Submitted (13-UUL-2002) Human Genome Sequencing Center, Department Submitted (13-UUL-2002) Human Genetics, Baylor College of Medicine, One Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA On Jul 12, 2002 this sequence version replaced gi:20303185.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequencing vector: Plasmid;
Chemistry: Dye-terminator Big Dye: 100% of reads
Assembly program: Phrap; version 0.990129
Consensus quality: 11965 bases at least Q40
Consensus quality: 119665 bases at least Q30
Consensus quality: 124966 bases at least Q20
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Contact: hgsc-help@bcm.tmc.edu
------ Project Information
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316 G

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Mammalia; Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Bibrecht, A., Chen, Y., Cullinan, C.A., Hayes, N., Leibowitz, M.D., Moller, D.E. and Berger, J.

Molecular cloning, expression and characterization of human peroxisome proliferator activated receptors gamma 1 and gamma 2 (bases 1 to 1518)

Elbracht, A., Chen, Y., Cullinan, C.A., Hayes, N., Leibowitz, M.D., Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (10-JUL-1996) Molecular Endocrinology, merck Research Labs., P.O. Box 2000, Mail Drop R80Y-265, Rahway, NJ 07060, USA Location/Qualifiers
Gaps
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                                                                                                                                      Db 108304 TACCCCGTGGGCCCAAGAATGACCATGGAAAACACA 108269
                                                                            6 TACCCCGTGGTGGCAGAATGACCATGGTTGACACA 41
0; Mismatches
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Search completed: January 21, 2003, 23:53:11 Job time : 1029.33 secs

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PAX8e8-PPARgammael Human PAX8e8-PPARg Human PPAR gamma P Human PPAR-gamma g

Human full-length

Human PPAR-gamma g Human PPAR gamma P Body weight gain i Human PPAR-gamma i Human PPAR-gamma i

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Human colon tumour Human colon cancer ovarian canc

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Human

Human bone marrow Probe #6339 used t Human genome-deriv

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PAX8-PPARgammal; oncogene; cytostatic; PAX8; PPARgammal; cancer; follicular carcinoma; PAX8e7-PPARgammael; human; ss.
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ABS19088
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14-AUG-2000; 2000US-0225079.
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Human PAX86-PPARG
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           GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
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PPARgammal, where the disorder is cancer, e.g. follicular carcinoma. The PAX8-PPARgammal molecules are also useful for providing nucleotide and amino acid sequences useful for detecting the above disease. The present sequence represents a human PAX867-PPARgammael polypeptide
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       PAX8-PPARgammal polypeptides can be expressed by standard recombinant
                  methodology. A PPARqamma ligand or agent is useful for treating a subject having a disorder characterized by the presence of a PAX8-PPARgammal, where the disorder is cancer, e.g. follicular carcinoma.
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                                                                                                                                                                                                        Length 2334;
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                                                                                                                                                                 Sequence 2334 BP; 614 A; 650 C; 573 G; 497 T; 0 other;
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                                                                                                                                                                                                                                                                              42
                                                                                                                                                                                                       Score 42; DB 22;
Pred. No. 2.1e-07;
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                                                                                                                                   encoding cDNA.
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                                                    New PAX8-PPARcl oncogene and oncoprotein, useful for detecting and treating certain tumors or cancers, e.g. follicular carcinoma
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 AGACCTACCCCGTGGTGGCAGAATGACCATGGTTGACACAG
                                                                                                                                                                                                                                                                                                                                                           Sequance 42 BP; 12 A; 11 C; 12 G; 7 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human PAX8e7-PPARgammael cDNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (BGHM ) BRIGHAM & WOMENS HOSPITAL INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 1; Page 100-104; 145pp; English
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                                                                                                           Claim 21; Page 118; 145pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAH76281 standard; cDNA; 2334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              18-JAN-2001; 2001WO-US01664.
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14-AUG-2000; 2000US-0225079,
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/*tag=
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WPI; 2001-514487/56.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first
                                                                                                                                                                                                                                                                                                                                                                                                                Best Loval Similarity
Matches 42; Conserv
                  P-PSDB; AAB85796
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 P-PSDB; AAB85793
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                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 2
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Query Match

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Subject having a disorder characterized by the presence of a PAX8-PPARgammal, where the disorder is cancer e.g. follicular carcinoma the PAX8-PPARgammal molecules are also useful for providing nucleotide and amino acid sequences useful for detecting the above disease. The present sequence represents a human PAX889-PPARgammael polypeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to an oncogene designated PAX8-PPARgammal that contains a PAX8 coding region fused to PPARgammal coding region. The PAX8-PPARgammal polypeptides can be expressed by standard recombinant methodology. A PPARgamma ligand or agent is useful for treating a
                                                                                                                                                            PAX8-PPARgammal; oncogene; cytostatic; PAX8; PPARgammal; cancer; follicular carcinoma; PAX8e9-PPARgammael; human; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             72.4%; Score 30.4; DB 22; Length 2625; 96.9%; Pred. No. 0.013;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nuclear receptor agonist; antagonist; identification; PPAR; peroxisome proliferator activated receptor; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 2625 BP; 662 A; 761 C; 646 G; 556 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1179 CATGGTGGCAGAAATGACCATGGTTGACACAG 1210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New PAX8-PPARc1 oncogene and oncoprotein,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           treating certain tumors or cancers, e.g.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         11 CGTGGTGGCAGAATGACCATGGTTGACACAG 42
                                                                                                                      Human PAX8e9-PPARgammael cDNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (BGHM ) BRIGHAM & WOMENS HOSPITAL INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 1; Page 112-116; 145pp; English.
                                                                                                                                                                                                                                                            Location/Qualifiers
1..2625
/*tag= a
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  AAH76283 standard; cDNA; 2625 BP.
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                                                                                                                                                                                                                                                                                                                                                                                                                     18-JAN-2001; 2001WO-US01664.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Fletcher JA;
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nes 31; Conserv
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                                                                                                                                                                                                                                                                                                                                       WO200152789-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    encoding cDNA.
                                                                                                                                                                                                                       Homo sapiens
                                                                                 29-0CT-2001
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                                          AAH76283;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAX36522;
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                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Vew PAX8-PPARc1 oncogene and oncoprotein, useful for detecting and creating certain tumors or cancers, e.g. follicular carcinoma
                                                                                                                                                                                                                                                                                                                                                                      PAX8-PPARgammal; oncogene; cytostatic; PAX8; PPARgammal; cancer; follicular carcinoma; PAX8e9(-exon 8)-PPARgammael; human; ss.
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Pred. No. 0.013;
72.4%; Score 30.4; DB 22; Length 42; 96.9%; Pred. No. 0.0052; Live 0; Mismatches 1; Indels C
                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 2596 BP; 660 A; 745 C; 672 G; 519 T; 0 other;
                                                                                                                                                                                                                                                                                                                               uman PAX8e9(-exon 8)-PARgammael cDNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1150 CATGGTGGCAGAATGACCATGGTTGACACAG 1181
                                                                                                       11 CATGGTGGCAGAAATGACCATGGTTGACACAG 42
                                                                             CGTGGTGGCAGAATGACCATGGTTGACACAG 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CGTGGTGGCAGAATGACCATGGTTGACACAG 42
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 1; Page 127-131; 145pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
161..2596
                                                                                                                                                                                                                   BP.
                                                                                                                                                                                                             AAH76294 standard; cDNA; 2596
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96.9%;
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14-AUG-2000; 2000US-0225079.
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                                                                                                                                                                                                                                                                                           (first entry)
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1es 31, Conservative
                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       polypeptide encoding cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /*tag=
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                Best Local Similarity
Matches 31; Conserv
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26-JUL-2001

Key

AAH76294;

Kroll TG,

Query Match

Matches 11

8

RESULT 5 AAH76283

, useful for detecting and follicular carcinoma

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Gaps

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The invention relates to a novel method for diagnosing and detecting the progression of liver cancer, hepatocellular carcinoma or metastatic liver tumour in a patient, and differentiating metastatic liver cancer from hepatocellular carcinoma in a patient, involving detecting the level of expression of two or more genes represented in ABN93503-ABN97455 in a tissue sample. The method of the invention has hepatocropic, and everyostatic activity. The method is useful for diagnosing and detecting the progression of liver cancer, hepatocellular carcinoma and metastatic
                                                                                                            The invention relates to an oncogene designated PAX8-PPARgammal that contains a PAX8 coding region fused to PPARgammal coding region. The PAX8-PPARgammal polypeptides can be expressed by standard recombinant methodology. A PPARgammal ligand or agent is useful for treating a subject having a disorder characterized by the presence of a PAX8-PPARgammal, where the disorder is cancer, e.g. follicular carcinoma. The PAX8-PPARgammal molecules are also useful for providing nucleotide and amino acid sequences useful for detecting the above disease. The present sequence represents a human PPARgamma polypeptide encoding cDNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gene, liver carcer, ds, hepatocellular carcinoma, hepatotropic, metastatic liver tumour, cytostatic; expression profile, disease state, disease progression, drug toxicity, drug efficacy, drug metabolism.
                                  New PAX8-PPARc1 oncogene and oncoprotein, useful for detecting and treating certain tumors or cancers, e.g. follicular carcinoma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Diagnosing and detecting the progression of liver cancer, hepatocellular carcinoma or metastatic liver tumor in a patient, involves detecting the level of expression of two or more genes
                                                                                                                                                                                                                                                                                                            Score 30.2; DB 22; Length 1811; Pred. No. 0.014; 0; Mismatches 3; Indels 0;
                                                                                                                                                                                                                                                                               Sequence 1811 BP; 510 A; 433 C; 422 G; 446 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Vockley JG;
                                                                                                                                                                                                                                                                                                                                                                                                 157 CGCCGTGGCCGCAGAAATGACCATGGTTGACACAG 191
                                                                                                                                                                                                                                                                                                                                                                                8 CCCCGTGGTGGCAGAATGACCATGGTTGACACAG 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gene #2212 used to diagnose liver cancer.
                                                                              Disclosure; Page 137-139; 145pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Peres-Da-Silva S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 1; SEQ ID NO 2212; 298pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ABN95714 standard; DNA; 1811 BP
                                                                                                                                                                                                                                                                                                               71.9%,
91.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             02-OCT-2001; 2001WO-US30589.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              13-AUG-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                32; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (GENE-) GENE LOGIC INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Horne D, Alvares C,
                                                                                                                                                                                                                                                                                                                                Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              liver tissue sample
     P-PSDB; AAB85802.
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                                                                                                                                                                                                                                                                                                               Query Match
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ABN95714
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                                                                                                                                                                                                                                                                                                                                                                                            agonists and antagonists comprises measuring fluorescent resonance energy transfer between fluorescent-labelled nuclear receptors and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                           co-activators. The method can be used for identifying agonists and antagonist of nuclear receptors.
                                                                                                                                                                                                                                                                                                                                                            receptor-gammal (PPAR-gammal).
The invention relates to a method for identifying nuclear receptor
                                                                                                                                                                                                                                                                                                                                            the human peroxisome proliferator activated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PAX8-PPARgammal; oncogene; cytostatic; PAX8; PPARgammal; cancer; follicular carcinoma; PPARgamma; human; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 71.9%; Score 30.2; DB 20; Length 1811; Best Local Similarity 91.4%; Pred. No. 0.014; Matches 32; Conservative 0; Mismatches 3; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 1811 BP; 510 A; 433 C; 422 G; 446 T; 0 other;
                                                                                                                                                                                                                                                                               Identifying nuclear receptor agonists and antagonists
                                                                                                                                                                                              Shou G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              157 CGCCGTGGCCGCAAAATGACCATGGTTGACACAG 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             8 CCCCGTGGTGGCAGAATGACCATGGTTGACACAG 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (BGHM ) BRIGHAM & WOMENS HOSPITAL INC.
                                                                                                                                                                                              Moller DE,
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173..1609
/*tag= a
                                                                                                                                                                                                                                                                                                             Disclosure; Fig 9b; 60pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ВР
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                                                                                                98WO-US21049
                                                                                                                              97US-0061385
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14-AUG-2000; 2000US-0225079.
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                                                                                                                                                                                              Cummings RT, Hermes JD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Fletcher JA;
                                                                                                                                                               (MERI ) MERCK & CO INC
                                                                                                                                                                                                                                                                                                                                              This sequence encodes
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                                                                                                                                                                                                                               WPI; 1999-263998/22.
                                                                                                                                                                                                                                           P-PSDB; AAY05471
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                                                                                                                              07-OCT-1997;
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 Homo sapiens
                              WO9918124-A1
                                                                                                06-OCT-1998;
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        Matches
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0
                                               drug toxicity, drug efficacy and drug metabolism.

Note: The sequence data for this patent did not form part of the plinted specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
liver carcinoma in a patient. The method is useful for identifying expression profiles which serve as useful diagnostic markers as well as markers that can be used to monitor disease states, disease progression,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   receptor gamma (PPPR-gamma) polypeptide. PPPR are orphan receptors, and may play a role in proliferative and differentiation aspects of cancer. The PPAR-gamma polynucleotide is useful for detecting a mRNA transcript that encodes PPAR polypeptide. It is also useful for detecting hybrid formation. The PPAR-gamma polypeptide is useful in diagnostics, drug
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present sequence encodes a human peroxisome proliferator-activated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /product= "peroxisome proliferator-activated receptor
                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Novel isolated and purified polynuclectide encoding human peroxisome proliferator-activated receptor gamma polypeptide useful in diagnostics, drug design and therapeutics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human; peroxisome proliferator-activated receptor gamma; PPAR-gamma;
                                                                                                                                                                                                    0
                                                                                                                                                                  DB 24; Length 1811;
                                                                                                                                                                                                                                                                                                                                                                                                                                            Human peroxisome proliferator-activated receptor gamma DNA.
                                                                                                                                                                                                  Indels
                                                                                                                                Sequence 1811 BP; 510 A; 433 C; 422 G; 446 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 1844 BP; 543 A; 433 C; 421 G; 447 T; 0 other;
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                                                                                                                                                              Score 30.2; DB 2
Pred. No. 0.014;
0; Mismatches
                                                                                                                                                                                                                                                              157 dececededaaardacarderreacacag 191
                                                                                                                                                                                                                             CCCCGTGGTGGCAGAATGACCATGGTTGACACAG 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 3; Column 43-48; 29pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
179..1609
                                                                                                                                                                                                                                                                                                                                           AAFS5663 standard; DNA; 1844 BP
                                                                                                                                                                ch 71.9%;
l Similarity 91.4%;
32; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 receptor; cancer; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          93US-0134557
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                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Blumberg B;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2001-234517/24.
                                                                                                                                                                Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          08-OCT-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                             AAF55663;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               orphan
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Matches
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Score 30.2; DB 22; Length 1844; Pred. No. 0.014;

71.9%; 91.4%;

Query Match Best Local Similarity

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Sequences AAS44576-AAS44919 represent full-length polynucleotides and contig polynucleotides encoding polypeptides of the invention. The DNA and protein sequences are useful for the treatment, diagnosis and and protein sequences are useful for the treatment, diagnosis and prevention of various types of disorder in a mammalian subject such as a such as leukemia, lymphona and neuroblastoma, autoimmune disorders such as multiple sclerosis, connective tissue disease, rheumatoid arthritis, disorders such as Parkinson's disease, Alzheimer's disease, Huntington's chorea, amyotrophic lateral sclerosis, spinal muscular atrophy and wernicke disease, inflammatory disorders such as nephritis, Crohn's wernicke disease, inflammatory disorders such as nephritis, Crohn's disease. The sequences exhibit activity relating to angiogenesis, cell proliferation, cell differentiation, stem cell growth factor, activin or inhibin. Therefore, they can be used to manipulate stem cells
                                                                                                                                                                                                                                                                                      Mammal, human; rhesus monkey; baker's yeast; fission yeast; Norway rat; mouse; Chinese hamster; African clawed frog; fruit fly; dog; leukaemia; cancer; lymphoma; neuroblastoma; autoimmune disorder; cell proliferation; nervous system disorder; inflammatory disorder; cell differentiation; disorders; stem cell growth factor; activin; inhibin; cartilage; burn; generic disorder; bone regeneration; tendon; ligament; tissue repair; cytostatic; antirheumatic; antiathritic; vulnerary; antiinflammatory; antibacterial; immunosuppressive; vasotropic; antiparkinsonian; neuroprotective; osteopathic; antidialsectiantiathmatic; antiathritic; immunostimulant; analgesic; gene tl rapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    prepared from various human tissues, for diagnosis, treatment of cancer, neurological, inflammatory disorders and for use in arrays for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Zhang J, Zhao QA, Ren F;
Ma Y, Wang D, Chen R, Xu C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Novel polypeptides and nucleic acids obtained from cDNA libraries
                                                                                                                                                                                                                                                        Human full-length polynucleotide sequence #78.
                                157 CGCCGTGGCCGCAGAATGACCATGGTTGACACAG 191
8 CCCCGTGGTGGCAGAATGACCATGGTTGACACAG 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Asundi V,
T, Wang J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 1; SEQ ID No 78; 153pp; English.
                                                                                                                                          BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Zhou P, As
Wehrman T,
                                                                                                                                      AAS44653 standard; DNA; 2295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   28-FEB-2000; 2000US-0515126.
18-MAX-2000; 2000US-0577409.
17-JUN-2000; 2000US-0597707.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              26-FEB-2001; 2001WO-US04926
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                                                                                                                                                                                                                 (first entry)
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Xue AJ, Yang Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             P-PSDB; AAU27753
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens.
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17-JUN-2000;
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19-SEP-2000;
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Best Local Similarity

Matches

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in culture to give rise to neuroepithelial cells that can be used to augment or replace cells damaged by illness, accidental damage or genetic disorders. The sequences may also be used for regeneration of bone, cartilage, tendons and ligaments and in tissue repair and burn healing.
                                                                        Note: Some sequences for this patent did not form part of the printed specification, but were obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention relates to an oncogene designated PAX8-PPARgammal that contains a PAX8 coding region fused to PPARgammal coding region. The PAX8-PPARgammal polypeptides can be expressed by standard recombinant methodology. A PPARgamma ligand or agent is useful for treating a subject having a disorder characterized by the presence of a PAX8-PPARgammal, where the disorder is cancer, e.g. follicular carcinoma. The PAX8-PPARgammal molecules are also useful for providing nucleotide and amino acid sequences useful for detecting the above disease. The present sequence represents the nucleotide sequence including and surrounding the fusion juncture in the PAX8e8-PPARgammael DNA.
                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New PAX8-PPARcl oncogene and oncoprotein, useful for detecting and treating certain tumors or cancers, e.g. follicular carcinoma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PAX8-PPARgammal; oncogene; cytostatic; PAX8; PPARgammal; cancer;
                                                                                                                                                                                  Match 71.9%; Score 30.2; DB 22; Length 2295; Local Similarity 91.4%; Pred. No. 0.015; Local Sies 32; Conservative 0; Mismatches 3; Indels 0;
                                                                                                                                               Sequence 2295 BP; 525 A; 606 C; 565 G; 599 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         follicular carcinoma; PAX8e8-PPARgammae1; human; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PAX8e8-PPARgammael fusion juncture DNA sequence.
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                                                                                                                                                                                                                                                                                1655 CGCCGTGGCCGCAGAAATGACCATGGTTGACACAG 1621
                                                                                                                                                                                                                                                           42
                                                                                                                                                                                                                                                           CCCCGTGGTGGCAGAATGACCATGGTTGACAGAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 21; Page 118; 145pp; English.
                                                                                                                                                                                                                                                                                                                                                                                         ВР
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                                                                                                                                                                                                                                                                                                                                                                                         AAH76285 standard; DNA; 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
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Length 42;

60.0%; Score 25.2; DB 22;

Query Match

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 contains a PAX8 coding region fueed to PPARgammal coding region. The PAX8-PPARgammal polypeptides can be expressed by standard recombinant methodology. A PPARgamma ligand or agent is useful for treating a subject having a disorder characterized by the presence of a PAX8-PPARgammal, where the disorder is cancer, e.g. follicular carcinoma. The PAX8-PPARgammal molecules are also useful for providing nucleotide and amino acid sequences useful for detecting the above disease. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention relates to an oncogene designated PAX8-PPARgammal that
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                present sequence represents a human PAX8e8-PPARgammae1 polypeptide
                                                                                                                                                                                                                                              oncogene; cytostatic; PAX8; PPARgammal; cancer;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New PAX8-PPARc1 oncogene and oncoprotein, useful for detecting treating certain tumors or cancers, e.g. follicular carcinoma
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               Indels
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                                                                                                                                                                                                                                                           carcinoma; PAX8e8-PPARgammae1; human; ss.
              8;
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                                         42
                                                                  42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5 CTACCCCGTGGTGGCAGAATGACCATGGTTGACACAG 42
                                                          S CCAGGCCTCCTCTCAGAAATGACCATGGTTGACACAG
                                       5 CTACCCCGTGGTGGCAGAATGACCATGGTTGACAG
Pred. No. 0.7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Mismatches
                                                                                                                                                                                                                  Human PAX8e8-PPARgammae1 cDNA sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (BGHM ) BRIGHAM & WOMENS HOSPITAL INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 1; Page 106-109; 145pp; English
                                                                                                                                                                                                                                                                                                              Location/Qualifiers
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                                                                                                                                  AAH76282 standard; cDNA; 2523
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l Similarity 78.9%;
30; Conservative
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14-AUG-2000; 2000US-0225079.
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                                                                                                                                                                                       (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
                                                                                                                                                                                                                                             PAX8-PPARgammal;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            P-PSDB; AAB85794
                                                                                                                                                                                                                                                                                                                                                                  WO200152789-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                encoding cDNA
                                                                                                                                                                                       29-OCT-2001
                                                                                                                                                                                                                                                                                      Homo sapiens.
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                                                                                                                                                                                                                                                            follicular
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                                                                                                                                                             AAH76282;
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                                                                                                       RESULT 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 13
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ID AAZ5
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14-APR-2000

AAZ57563;

WO200001679-A1 lomo sapiens

30-JUN-1999; 01-JUL-1998;

13-JAN-2000

Sugiyama Y,

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5-Nembered N-heterocyclic derivatives useful for preventing or treating diabetes mellitus, hyperlipidaemia or impaired glucose tolerance
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human, PPAR gamma, RXR alpha, PPRE, herpes simplex virus, HSV, thymidine kinase minimum promoter; retinoid X receptor; antidiabetic; peroxisome proliferation-activated receptor; neuroprotective; muscular; nephrotropic; ophthalmological; osteopachic; antilipemic; hypotensive; immunosuppressive; cytostatic; antibacterial; anti-HIV; endocrine;
                    PPAR-gamma; peroxisome proliferator-activated receptor gamma; human; hypodyroaemic; hypolipaemic; antidiabetic; antidiflammatory; antiarteriosclerotic; diabetes; hyperlipidaemia; glucose intolerance; PCR primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present sequence is that of primer PAG-U, which was used with primer PAG-L (see AAH36112) in the PCR amplification of human peroxisome proliferator-activated receptor gamma (PPAR-gamma) cDNA, using heart cDNA as template. The primers are based on the reported base sequence of the PPAR-gamma gene. PPAR-gamma is a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               novel 5-membered N-heterocyclic compounds having hypoglycaemic and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         hypolipidaemic action, making them useful as agents for preventing or treating diabetes mellitus, hyperlipidaemia, impaired glucose
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               expression is induced at a very early stage of adipose cell differentiation. PPAR-gamma forms a dimer with the retinoid X receptor (RAR) by binding to a ligand, and binds to a responsive site of a target gene in the nucleus to directly control (activat transcription. PPAR-gamma ligands suppress the production of inflammatory cytokines by monocytes. The invention provides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          tolerance, inflammatory disease and arteriosclerosis. The no compounds have potent PPAR-gamma-RXR-alpha heterodimer ligand
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Odaka H, Kimura
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        12 GTGGTGGCAGAAATGACCATGGTTGACACAG 42
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Example 1; Page 85; 376pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Momose Y, Maekawa T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2001-432602/46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
                                                                                                                                                                                               WO200138325-A1.
                                                                                                                                                                                                                                                                                                                                          10-NOV-1999;
                                                                                                                                              Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                       10-DEC-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present invention describes retinoid associated receptor regulators comprising a 1,3-azole derivative (1). The retinoid associated receptor regulators are useful as insulin receptor binding agents for treating and preventing diabetes, hyperlipsemia and obesity. (1) may also be useful for the treatment and prevention of diabetic complications (e.g. nerve, kidney, retina, blood vessel and bone narrowing disorders and diseases), osteoporosis, cadhexia (e.g. due to cancer, diabetes or vascular disorders) fatty liver hypertension, polycystic ovary yndrome, kidney disorders (e.g. glomerulonephritis, diabetes or syndrome, kidney disorders (e.g. glomerulonephritis, diabetic chaptopathy and glomerulone x, cancer (e.g. leukaemia and breast cancer), and arteriosolerosis. The present sequence represents a PCR primer for infartiosolerosis. The present sequence represents a PCR primer for infartion which is used in the exemplification of the present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0;
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                                                                                                                                                                                                                                      cerebroprotective, antiarteriosclerotic, hyperlipaemia, osteoporosis, cachexia, cancer, vascular disorder; hypertension, kidney disorder; muscular dystrophy, cardiac infarction, angina pectoris, syndrome X; cerebral infarction, hyperinsulinaemia, leukaemia, arteriosclerosis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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anabolic; cytostatic; hypotensive; cardiant; antianginal; obesity;
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                                                                                                                                                             Retinoid associated receptor regulator; 1,3-azole; diabetes;
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                                                                                                            Human PPAR gamma PCR primer PAG-U SEQ ID NO:1.
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llarity 87.1%;
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(activate)

The novel

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Gaps

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27;

12 Matches

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Query Match Local AAH26111;

DXXXXX

RESULT 14 AAH2611

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cardiant; cerebroprotective, antiinflammatory; antiarthritic; antiulcer, antirheumatic; hepatotropic; respiratory; gastrointestinal; neuropathy; diabetic complication; nephropathy; retinopath; osteopathy; obesity; hypertension; cachexia; cancer; infection; AIDS; renal disorder; tumour; polycystic ovary syndrome; muscular dystrophy; myocardial infarction; cerebral vascular disorder; syndrome X; inflammatory disease; arteriosclerosis; PCR primer; ss.
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Homo sapiens.

WO200134579-A1.

17-MAY-2001

09-NOV-2000; 2000WO-JP07878.

99JP-0320318. 10-NOV-1999;

(TAKE ) TAKEDA CHEM IND LTD.

Kimura H; Odaka H, Momose Y, Imoto H,

WPI; 2001-355474/37.

Use of new and known alkoxyiminoalkanoic acid derivatives as peroxisome proliferation-activated receptor agonist like substances for treating e.g. diabetes

Example; Page 66; 92pp; Japanese.

endocrine, cardiant, cerebroprotective, antinfilamentory, antiarthritic, antirheumatic, hepatotropic, respiratory, antiuncer and gastrointestinal activities. (I) can be used for treating or preventing diabetic complications (such as neuropathy, nephropathy, retinopathy or osteopathy), obesity, hypertension, cachexia (e.g. due to cancer, infections or AIDS), polycystic ovary syndrome, renal disorders (e.g. qlomerulonephritis), muscular dystrophy, myocardial infarction, cerebral apoplexy), syndrome X, tumours, inflammatory diseases (e.g. chronic rheumatoid arthritis, hepatitis, pneumonia or ulcerative colitis) and arteriosclerosis. The present sequence represents a PCR primer for human PPAR gamma, which is used in an example from the present invention. alkoxyiminoalkanoic acid derivatives (I). Alkoxyiminoalkanoic acid derivatives and their salts and produces can be used for treating or preventing diabetes, hyperlipemia or impaired glucose tolerance or as a ligand for peroxisome proliferation-activated receptors (PPAR) or retinoid X receptors (RXR). (I) have antidiabetic, neuroprotective, nephrotropic, ophthalmological, osteopathic, antilipemic, hypotensive, muscular, immunosuppressive, cytostatic, antibacterial, anti-HIV, The present invention describes the use of new and known 

Sequence 33 BP; 10 A; 6 C; 11 G; 6 T; 0 other;

Gaps ; 0 Score 24.6; DB 22; Length 33; Pred. No. 1.2; Indels 4, 0; Mismatches 58.6%; 27; Conservative Query Match Best Local Similarity Matches

12 GTGGTGGCAGAATGACCATGGTTGACACAG 42 g

Search completed: January 21, 2003, 23:09:52 Job time : 130.667 secs

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GTGGGTACCGAAATGACCATGGTTGACACAG 31

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5: /cgn2 6/ptodata/1/ina/PcTUS COMB.seq:*
6: /cgn2_6/ptodata/1/ina/PcTUS COMB.seq:*
                 GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
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US-09-464-34-3

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US-08-917-653-4

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US-08-78-20-1

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US-08-724-394A-21

US-08-724-394A-21

US-08-124-344A-21

US-09-121-160-2

US-09-121-160-2

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                                                                                                                                                                                                                                                                Sequence:
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Sequence 1, Appli
Sequence 8, Appli
Sequence 4, Appli
Sequence 1, Appli
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Sequence 12, R
Sequence 12, R
Sequence 12, R
Sequence 12, R
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                                                       Sequence 4, A Sequence 18, Sequence 18,
                                           Sequence 4,
              Sequence
                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Greene, Marianne E.
APPLICANT: Blumberg, Bruce
TITLE OF INVENTION: Human Peroxisome Proliferator Activated
TITLE OF INVENTION: Receptor Gamma: Compositions and Methods
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSBE: Rockey, Milnamow & Katz, Ltd.
STREET: 2 Prudential Plaza, Suite 4700 180 N. Stetson
CITY: Chicago
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/134,557D
        US-09-226-741-2
US-09-555-514-2
US-09-559-514-4
US-09-559-514-4
US-09-559-514-4
US-08-59-514-4
US-08-59-518-18
US-08-389-928-18
US-08-311-959-12
US-08-932-0878-12
US-08-932-0878-12
US-08-932-0878-12
US-08-932-0878-12
US-08-932-0878-12
US-08-932-0878-12
US-08-932-0878-12
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US-08-841-349-8
US-08-766-858A-4
                                                                                                                                                                                                                                                                                AL1GNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION: 435
ATTORNEY AGENT INFORMATION:
NAME: Katz, Martin L.
REGISTRATION NUMBER: 25,011
REFERRINGE/DOCKET NUMBER: ARCH:098
TELECOMMUNICATION:
TELECOMMUNICATION: 312-616-5400.
                                                                                                                                                                                                                                                                                                                                               Sequence 1, Application US/08134557D; Patent No. 6200802; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: linear MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGIH: 1844 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: 312-616-5460
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                    nucleic acid
EDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 179..1606
USA
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STRANDEDNESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 60601
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US-08-134-557D-1
                                                                                                                                                                                                                                                                                                                                     US-08-134-557D-1
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COUNTRY:
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8 CCCCGTGGTGGCAGAATGACCATGGTTGACACAG 42

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Sequence 2 Sequence 1

Sequence

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APPLICANT: TANABE SETYAKU CO. LTD.
APPLICANT: TANABE SETYAKU CO. LTD.
APPLICANT: TANIGUCHI, TOMOYASU
APPLICANT: MICHAMI, UDIRKO
TITLE OF INVENTIONS: METHOD FOR IDENTIFYING OR SCREENING AGONIST AND ANTAGONIST TO STILE REPRENCE: TANIGUCHI=6
CURRENT APPLICATION NUMBER: US/09/514,247A
CURRENT FILING DATE: 1090-08-24
PRIOR APPLICATION NUMBER: PCT/JP98/03734
PRIOR APPLICATION NUMBER: JP231044/1997
PRIOR FILING DATE: 1997-08-27
PRIOR FILING DATE: 1997-08-27
PRIOR FILING DATE: 1997-08-27
SOFTWARE: Patentin version 3.0
SEQ ID NO 5
LENGTH...1679
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             54.8%; Score 23; DB 4; Length 1679;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Rosenfield, Robert L.
IIILE OF INVENTION: IDENTIFICATION OF ACTIVATORS AND
TITLE OF INVENTION: INHIBITORS OF SEBUM FORWATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: PROPER PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%; Pred. No. 1.2; ive 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 5, Application US/09514247A Patent No. 6365361
                                                                                                                                                                                                                                                                                                    171 AGAAATGACCATGGTTGACACAG 193
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; Sequence 4, Application US/08917653
; Patent No. 6004751
; GENERAL INFORMATION:
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, WI
                                                                       ; NAME/KEY: CDS
; LOCATION: (91) ...(1608)
US-09-484-345-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LOCATION: (159) .. (1679)
         TYPE: DNA ORGANISM: Homo sapiens FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity
Matches 23; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                             US-09-514-247A-5
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                                                                                                                                                                                       AL INFORMATION:
APPLICANT: SMICH, ROY G.
TITLE OF INVENTION: ANTIPROLIFERATIVE AGENTS ASSOCIATED WITH
PEROXISOME PROLIFERATOR ACTIVATED RECEPTORS GAMMAI AND GAMM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Robert McKay
APPLICANT: Robert McKay
APPLICANT: Alexander H. Borchers
APPLICANT: Alexander H. Borchers
APPLICANT: Alexander H. Borchers
APPLICANT: Brende F. Bake
APPLICANT: Brende F. Bake
TITLE OF INVENTION: ANTISENS
FILE REFERENCE: RTS-0104
FULE REFERENCE: RTS-0104
CURRENT PAPLICANTION NUMBER: US/09/484,345
NUMBER OF SEQ ID NOS: 90
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                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READBLE FORM:
MEDIUM TYPE: Ploppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: Power Macintosh 7500/100
SOFTWARE: Microsoft word 6.0
CURRENT APPLICATION DATA:
FILING DATE: 03-Aug-1998
CLASSIFICATION: CAMPI
                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
ADDRESSEE: Jack L. Tribble
STREET: 126 E. Lincoln Ave., P.O. Box 2000
157 GCCGTGGCCGCAGAAATGACCATGGTTGACACAG 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ALLONG Tribble, Jack L.
REGISTRATION NUMBER: 32,633
REFERENCE/DOCKET NUMBER: «Unknown»
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION (908) 594-5321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: 08/844,007
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
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MOLECULE TYPE: DNA (genomic)

SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-09-128-142-3
                                                                                   RESULT 2
US-09-128-142-3
Sequence 3, Application US/09128142
Patent No. 6294559
GENERAL INFORMATION:
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LENGTH: 1518 base pairs
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Patent No. 6159734
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            81 AGAAATGACCATGGTTGACACAG 103
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STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: (908) 594-
INFORMATION FOR SEQ ID NO: 3:
                                                                                                                                                                                                                                                                                                                                                                CITY: Rahway
STATE: New Jersey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity 100.
Matches 23; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY: US
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US-09-484-345-3
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120 AGAAATTACCAIGGTIGACACAG 142
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                                                                                                    US-08-325-426B-1
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                                                                              RESULT 7
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Pred. No. 3.8;
0; Mismatches 1; Indels (
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                                                                                                                                                                                                                                                                                                                                                                                                           1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 3, Application US/08917653
Patent No. 6004751
GENERAL INFORMATION:
APPLICANT: Rosenfield, Robert L.
TITLE OF INVENTION: IDENTIFICATION OF ACTIVATORS AND TITLE OF INVENTION: INHIBITORS OF SEBUM FORWATION NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRANT APPLICATION DATA:
APPLICATION NUMBER: US/08/917,653
FILING DATE: CONCURRENTLY HEREWITH
                                                                                          NAME: Highlander, Steven L.
REGISTRATION NUMBER: 37,642
REFERENCE/DOCKET NUMBER: ARCD:216
TELECOMMUNICATION INFORMATION:
TELEPHONE: (512) 418-3000
TELEPAX: (512) 44-7577
INDORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
                      APPLICATION NUMBER: US/08/917,653
FILING DATE: Concurrently Herewith
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ARCD:216
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CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Highlander, Steven L.
REGISTRATION NUMBER: 37,642
REFERENCE/DOCKET NUMBER: ARCD
TELECOMMUNICATION INFORMATION:
TELEPHONE: (512) 418-3000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   82 AGAATTACCATGGTTGACACAG 104
                                                                                                                                                                                                                                                                                                                                                                                                           0;
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                                                                                                                                                                                                                                                                                                                                                                      51.0%;
95.7%;
                                                        CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                               LENGTH: 277 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 95.7
Matches 22; Conservative
    CURRENT APPLICATION DATA:
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linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity
Matches 22; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CITY: Houston STATE: Texas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY: U.S. ZIP: 77210
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US-08-917-653-3
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20 AGAAATGACCATGGTTGACACAG 42

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GENERAL INFORMATION:
APPLICANT: Evans, Ronald M.
APPLICANT: Forman, Barry M.
TITLE OF INVENTION: MODULATORS OF PEROXISOME PROLIFERATOR
TITLE OF INVENTION: ACTIVATED RECEPTOR-GAMMA, AND METHODS FOR THE USE THEREOF
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
STREET: 144 South Flower Street, Suite 2000
CITY: Los Angeles
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0;
                                                                               GENERAL INCORMATION:
APPLICANT: PU, Jianlin
APPLICANT: TAN, Boon-Haun
APPLICANT: TAN, Bu-Hian
APPLICANT: TAN, TOW-Cheong
APPLICANT: TAN, Yow-Cheong
APPLICANT: TAN, Yin-Hwee
APPLICANT: TAN, YIN-HWE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    50.0%; Score 21; DB 3; Length 10718; 73.0%; Pred. No. 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IRW PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25 (BPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/325,426B
FILNG DATE: 16-DEC-1994
INPORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: linear MOLECULE TYPE: CDNA sequence corresponding to MOLECULE TYPE: the genomic RNA of DEN1-S275/90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4 CCTACCCGGGGGGGGAAATGACCATGGTTGACAC 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             8th FLOOR, 1100 NORTH GLEBE ROAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Dengue Fever Virus Type
STRAIN: $275/90
Sequence 1, Application US/08325426B Patent No. 6017535
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 1, Application US/09255392
Patent No. 6214850
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY: USA
ZIP: 22201-4714
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 10718 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 73.0°
Matches 27, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              81..10268
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                8
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ORIGINAL SOURCE:
ORGANISM: Deng
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: CDS
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us-09-765-111a-7.rni

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49.5%; Score 20.8; DB 2; Length 2005; 91.7%; Pred. No. 11;
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
COMPUTER: IEM PC compatible
COMPUTER: IEM PC compatible
COMPUTER: IEM PC compatible
COMPUTER: PATENTION BY STEM: PC-DOS/MS-DOS
SOFTWARE: PATENTION DATA:
CUREBNT APPLICATION NUMBER: US/08/477,493
FILING DATE: O7-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Reiter, Stephen E.
REJECKATION NUMBER: 31,192
REPERENCE/DOCKET NUMBER: P41 9958
TELECOMMUNICATION INPORMATION:
SEQUENCE CHAAGTERISTICS:
SEQUENCE CHAAGTERISTICS:
                        REGISTRATION NUMBER: 31,192
REFERENCE/DOCKET NUMBER: P41 9971
TELECOMMUNICATION INFORMATION:
FELEPHONE: 619-546-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           341 CTGAAATTACCATGGTTGACACAG 364
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                                                                                                                TELEFAX: 619-546-9392
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2005 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FRATURE:
FRATURE:
LOCATION: 352.1776
US-08-484-200-1
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STRANDEDNESS: both
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Best Local Similarity
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TOPOLOGY: bot
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; LOCATION:
US-08-477-493-1
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49.5%; Score 20.8; DB 4; Length 1796;
Best Local Similarity 91.7%; Pred. No. 11;
Marches 22; Conservative 0; Mismatches 2; Indels 0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: EVENAL, RONALD M.
APPLICANT: FORMAN, BARRY M.
APPLICANT: FORMAN, BARRY M.
APPLICANT: KLIEWER, SIEVEN A.
APPLICANT: MOSTELITA S.
TITLE OF INVENTION: NOVEL MEMBERS OF THE STEROID/THYROID
ITTLE OF INVENTION: SUPERFAMILY AND USES THEREFOR
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: PRETTY, SCHROEDER, BRUEGGEMANN & CLARK
STREET: 444 SOUTH FLOWER STREET, SUITE 2000
CITY: LOS ANGELES
STATE: CALIFORNIA
                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Ploppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/255,392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: Patentin Release #1.0, Version #1.25
CUBRENT APPLICATION DATA:
PPLICATION NUMBER: US/08/484,200
FILING DATE: 07-UUN-1995
                                                                                                                                                                                                                                                                      FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: US/08/477,493
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Reiter, Stephen E.
REGISTRATION NUMBER: 31,192
REFERENCE/FOCKET NUMBER: P41 9958
TELEPHONE: 619-546-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  341 CTGAAATTACCATGGTTGACACAG 364
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Sequence 1, Application US/08484200
Patent No. 5861274
GENERAL INFORMATION:
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ATTORNEY/AGENT INFORMATION:
NAME: REITER, STEPHEN E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ) NAME/KEY: CDS
; LOCATION: 352..1776
US-09-255-392-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: nucleic acid
STRANDEDNESS: both
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: both
MOLECULE TYPE: CDNA
             CA
USA
STATE: C. COUNTRY: USA 90071
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     90071
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US-08-477-493-1
Sequence 1, Application US/08477493
Sequence 1, Application US/08477493
Patent No. 593442
GENERAL INFORMATION:
APPLICANT: Evans, Ronald M.
APPLICANT: Forman, Barry M.
TITLE OF INVENTION: MODULATORS OF PEROXISOME PROLIFERATOR
TITLE OF INVENTION: ACTIVATED RECEPTOR-GAMMA, AND METHODS FOR THE USE THEREOF
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSE: Pretty, Schroeder, Brueggemann & Clark
STREET: 444 South Flower Street, Suite 2000
                                                                            0
                                                                        Gaps
                                                                     0;
Query Match
49.5%; Score 20.8; DB 2; Length 2005;
Best Local Similarity 91.7%; Pred. No. 11;
Matches 22; Conservative 0; Mismatches 2; Indels 0
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341 CTGAAATTACCATGGTTGACACAG 364

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Gaps

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Indels

2;

0; Mismatches

19 CAGAAATGACCATGGTTGACACAG 42

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22; Conservative

Matches

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Gaps
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                                                                                                                              APPLICANT: Krommal, Gregory S.
APPLICANT: Lauter, Peter M.
APPLICANT: Lauter, Peter M.
APPLICANT: Raddy, David A.
APPLICANT: Tranchinash, Zenta
APPLICANT: Tranchinash, Zenta
APPLICANT: Wolff, Roger K.
TITLE OF INVENTION: Megabase Transcript Map: No. 5872237e1
TITLE OF INVENTION: Sequences and Antibodies Thereto
CORRESPONDENCES: 31
CORRESPONDENCES: 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY: USA
ZIP: 9411-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/724,394A
FILING DATE: 01-OCT-1996
CLASSIFICATION: 536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Db 35492 ATACTCACAGGGTCCTTGGAGAATGACGATTGTCCACA 35530
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                                                                                                                                                                                                                                                                                                                                                                ADDRESSE: TOWNSEND and TOWNSEND and CREW STREET: Two Embarcadero Center, 8th Floor CITY: San Francisco STATE: CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 19.8; DB Pred. No. 89; 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 AGACCTACCCCGTGGTGGCAGAAATGACCATGGTTGACA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FEATURE:
NAME/KEY: misc_feature
LOCATION: 1..246240
OTHER INFORMATION: /note= "HLA-H.CONTIG"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Fitts, Renea A.
REGISTRATION NUMBER: 35,136
REFERENCE/DOCKET NUMBER: 017957-000100
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-576.0200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; Sequence 21, Application US/08724394A
; Patent NO. 5872237
GENERAL INFORMATION:
; APPLICANT: Feder, John N.
; APPLICANT: Kronmal, Gregory S.
; APPLICANT: Ruddy, David A.
; APPLICANT: Ruddy, David A.
; APPLICANT: Thomas, Winscon
                                    Sequence 20, Application US/08724394A
Patent No. 2872237
GENERAL INFORMATION:
APPLICANT: Feder, John N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: 415-576-0300
INFORMATION FOR SEQ ID NO: 20.
SEQUENCE CHARACTERISTICS:
LENGTH: 246240 base pairs
TYPE: nucleic acid
STRANDEDNESS: not relevant
TOPOLOGY: not relevant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               47.18;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 69.23
Matches 27; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-08-724-394A-20
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US-08-724-394A-21
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                                                                                                                                                           GENERAL INFORMATION:
APPLICANT: Evans, Ronald M.
APPLICANT: Evans, Ronald M.
TITLE OF INVENTION: SELECTIVE MODULATORS OF PEROXISOME
TITLE OF INVENTION: PROLIFERATOR ACTIVATED RECEPTOR-GAMMA, AND METHODS FOR THE
TITLE OF INVENTION: USE THRREOF
TERRENCE: SALK1470-1
CURRENT PILING DATE: 1995-06-05
EARLIER PILING DATE: 1995-04-25
NUMBER OF SEQ ID NOS: 7
SOFTWARE: FRESEQ for Windows Version 4.0
SEQ ID NO 1
LENGTH: 2005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: EVANA, Ronald
APPLICANT: EVANS, Ronald
APPLICANT: EVANS, Ronald
APPLICANT: EVANS, Ronald
APPLICANT: PORMAN, BATY
TITLE OF INVENTION: MODULATORS OF PEROXISOME PROLIFERATOR ACTIVATED RECEPTOR-GAMMA,
TITLE OF INVENTION: AND METHODS FOR THE USE THEREOF
FILE REPREBRUCE: SALK1480-2
CURRENT APPLICATION NUMBER: US 09/9788,070
CURRENT FILING DATE: 1099-02-22
NUMBER OF SEQ ID NOS: 7
SOFTWARE: PATENTION OF SEQ ID NOS: 7
SOFTWARE: LENGTH: 2005
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ch 49.5%; Score 20.8; DB 3; Length 2005; 1 Similarity 91.7%; Pred. No. 11; 22; Conservative 0; Mismatches 2; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ch 49.5%; Score 20.8; DB 4; Length 2005; 1 Similarity 91.7%; Pred. No. 11; 22; Conservative 0; Mismatches 2; Indels 0.
341 CTGAAATTACCATGGTTGACACAG 364
                                                                                                                    Sequence 1, Application US/08465375A
Patent No. 6022897
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             341 CTGAAATTACCATGGTTGACACAG 364
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 12
US-09-788-070-1
; uence 1, Application US/09788070
; art No. 6413994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              19 CAGAAATGACCATGGTTGACACAG 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: CDS
LOCATION: (352)...(1776)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: DNA
ORGANISM: Mus musculus
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; LOCATION: (352)..(1776)
US-09-788-070-1
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ORGANISM: Mus Musculus
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Matches 22; Conserv
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Matches 22; Conserv
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                                                                         RESULT 11
US-08-465-375-1
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US-08-724-394A-22
Sequence 22, Application US/08724394A
Sequence 22, Application US/08724394A
Patent No. 587237
GENERAL INFORMATION:
APPLICANT: Feder, John N.
APPLICANT: Ruddy, David A.
APPLICANT: Thomas, Winston
APPLICANT: Thomas, Winston
APPLICANT: Touchihashi, Zenta
APPLICANT: Wolff, Roger K.
TITLE OF INVENTION: Regabase Transcript Map: No. 5872237el
TITLE OF INVENTION: Sequences and Antibodies Thereto
NUMBER OF SECUENCES: 31
CORRESPONDENCE ADDRESS: ADDRESSE: TOWNSEND and CREW LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 47.1%; Score 19.8; DB 2; Length 246240; Best Local Similarity 69.2%; Pred. No. 89; Matches 27; Conservative 0; Mismatches 12; Indels 0;
APPLICANT: Tsuchihashi, Zenta
APPLICANT: Wolff, Roger K.
TITLE OF INVENTION: Megabase Transcript Map: No. 5872237e1
TITLE OF INVENTION: Sequences and Antibodies Thereto
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
ADDRESSEE: TOWNSEND and TOWNSEND and CREW LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: CA
                                                                                                                                                                                                                                                                COMPUTRY: USA
COMPUTRY READABLE PORM:
MEDIUM TYPE: Floppy disk
COMPUTRS: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/724,394A
FILING DATE: 01-OCT-1996
CLASSIFICATION: 536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Db 35492 ATACTCACAGCGTCCTTGGAGAAATGACCATTGTCCACA 35530
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: misc feature
LOCATION: 1..246240
OTHER INFORMATION: /note= "HLA-H.CONTIG"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    017957-000100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
NAME: Fitts, Renee A.
REGISTRATION NUMBER: 35,136
REFERENCE/DOCKET NUMBER: 01795
TELEPHONE: 415-576-0200
TELEPHONE: 415-576-0300
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
LENGTH: 246240 base pairs
TYPE: nucleic acid
STRANDEDRES: not relevant
TOPOLOGY: not relevant
MOLECULE TYPE: CDNA
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COMPUTER READABLE FORM:
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Gaps
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                                   COMPUTER: IBM PC compatible
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/724,394A
FILING DATE: 01-0CT-1996
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Filts, Renee A.
REGISTRATION NUMBER: 017957-000100
TELEFAN: 415-576-0200
TELEFAN: 415-576-0300
TELEFAN: 415-576-0300
TELEFAN: 415-576-0300
TELEFAN: 415-576-0300
TELEFAN: 415-576-0300
TELEFAN: 416-576-0300
TELEFAN: 416-676-0300
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; LOCATION: 1..246240
US-08-724-394A.22
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       Floppy disk
MEDIUM TYPE:
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TYPE: DNA
ORGANISM: Homo Sapiens
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Best Local Similarity
' .hag 42; Conserva
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US-09-765-111A-7
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US-09-765-111A-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 2
US-09-765-111A-1
                                                                                          LENGTH:
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Sequence 11, Appli
Sequence 5, Appli
Sequence 22, Appli
Sequence 2212, Appli
Sequence 9, Appli
Sequence 9, Appli
Sequence 15, Appli
Sequence 15, Appli
Sequence 15, Appli
Sequence 15, Appli
Sequence 990, Appli
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Sequence 109, Appli
Sequence 109, Appli
Sequence 109, Appli
Sequence 119, Appli
Sequence 12, Appli
Sequence 12, Appli
Sequence 13, Appli
Sequence 13, Appli
Sequence 13, Appli
Sequence 14, Appli
Sequence 14, Appli
Sequence 15, Appli
Sequence 24, Appli
Sequence 24, Appli
Sequence 24, Appli
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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                                                                                                                                                                                                                                                                                  1 agacctaccccgtggtggca.....aatgaccatggttgacacag
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/cgn2_6/ptodata1/pubpna/PCT_NEW_PUB.seq:*
/cgn2_6/ptodata1/pubpna/PCT_NEW_PUB.seq:*
/cgn2_6/ptodata1/pubpna/USO6_NEW_PUB.seq:*
/cgn2_6/ptodata1/pubpna/USO6_NEW_PUB.seq:*
/cgn2_6/ptodata1/pubpna/USO8_NEW_PUB.seq:*
/cgn2_6/ptodata1/pubpna/USO8_NEW_PUB.seq:*
/cgn2_6/ptodata1/pubpna/USO8_PUBCOMB.seq:*
/cgn2_6/ptodata1/pubpna/USO8_PUBCOMB.seq:*
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/cgn2_6/ptodata1/pubpna/USO9_NEW_PUB.seq:*
/cgn2_6/ptodata1/pubpna/USO9_NEW_PUB.seq:*
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/cgn2_6/ptodata1/pubpna/USO0_NEW_PUB.seq:*
/cgn2_6/ptodata1/pubpna/USO0_NEW_PUB.seq:*
/cgn2_6/ptodata1/pubpna/USO0_NEW_PUB.seq:*
/cgn2_6/ptodata1/pubpna/USO0_NEW_PUB.seq:*
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/cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:
GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
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US-09-765-111A-1
US-09-765-111A-2
US-09-765-111A-2
US-09-765-111A-2
US-09-765-111A-2
US-09-765-111A-2
US-09-8080-107-2212
US-09-816-828-9
US-09-816-828-9
US-09-765-111A-9
US-09-765-111A-3
US-09-765-111A-3
US-09-765-111A-15
US-09-765-111A-15
US-10-109-886-5
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US-09-867-701-6261
US-09-765-111A-13
US-09-765-111A-24
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                                                                                                                                                                                                                                                                                                                                                                                                393868 segs, 222934149 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SUMMARIES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                        - nucleic search, using sw model
                                                                                                                                         January 21, 2003, 23:59:20
                                                                                                                                                                                                                                                                                                                            IDENTITY NUC
Gapop 10.0 , Gapext 1.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Minimum DB seq length: 0
Maximum DB seq length: 200000000
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Match Length DB
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2625
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Perfect score:
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                                                                                                                                         Run on:
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20 21.6 51.4 167 10 US-09-864-761-27653 Sequence 27653, A 2 21.6 51.4 455 10 US-09-864-761-1018 Sequence 27653, A 4 25 10 US-10-044-090-587 Sequence 587, App 22 21.6 51.4 3305 12 US-10-044-090-587 Sequence 587, App 22 20.8 49.5 2793 9 US-10-9270-884 Sequence 1. Appli Sequence 2. Appli Sequence 2. Appli Sequence 2. Appli Sequence 3. Ap
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## NGENE TO

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US-09-765-111A-7

US-09-765-111A-7

US-09-05-765-111A-7

US-0020106796A1

PRICE NO. US20020106796A1

PRICE NO. US20020106796A1

APPLICANT: PLOCH TOOM

APPLICANT: FAD1, TooM GA

TITLE OF INVENTION: PAXS-PPARgamma NUCLEIC ACID MOLECULES

TITLE OF INVENTION: DOUBER: US-09/765,111A

CURRENT FILING DATE: 2000-01-18

PRIOR PRILING DATE: 2000-01-20

PRIOR FILING DATE: 2000-01-4

NUMBER OF SEA DO NOS: 47

SOFTWARE: FastSEQ for Windows Version 3.0

ENGRANGE PASSED NOS

SOFTWARE: PAXS-SEA DOUBLES

PRIOR FILING DATE: 2000-01-4

NUMBER OF SEA DO NOS: 47

CORGANISM: Homo Sapiens

PRATURE:

NAME/FX: COR

CORGANISM: Homo Sapiens

MATCHES AD11A-7

QUERY MATCH

Best Local Similarity 100.0%; Pred: No. 2.1e-08;

MATCHES AD2 ON SEA DOUBLES

MATCHES AD2 ON SEA DOUBLES

MATCHES AD3 ON SEA DOUBLES

MATCHES AD4 ON SEA DOUBLES

MATCHES AD5 ON
```

us-09-765-111a-7.rnpb

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Query Match 72.4%; Score 30.4; DB 10; Length 2596; Best Local Similarity 96.9%; Pred. No. 0.0028; Matches 31; Conservative 0; Mismatches 1; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                72.4%; Score 30.4; DB 10; Length 2625; 96.9%; Pred. No. 0.0028; trive 0; Mismatches 1; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 5. Application US/09765111A
Patent No. US2002016796A1
GENERAL INFORMATION:
APPLICANT: Flecther, Jonathan A.
APPLICANT: Factor, Jonathan A.
APPLICANT: Rxoll, Todd G.
TITLE OF INVENTION: PAX8-PEARgamma NUCLEIC ACID MOLECULES
TITLE OF INVENTION: NAND POLYPEPTIDES AND USES THEREOF
FILE REFERENCE: B0801/7196/ERP/MAT
CURRENT APPLICATION NUMBER: US/09/765,111A
CURPENT FILING DATE: 2001-01-18
PRIOR APPLICATION NUMBER: US 60/177,109
PRIOR APPLICATION NUMBER: US 60/177,109
PRIOR APPLICATION NUMBER: US 60/225,079
PRIOR PRING DATE: 2000-08-14
NUMBER OF SEQ ID NOS: 47
SOFTWARE PRACES FRANCE SO00-08-14
SEQ ID NO 5:
LENGTH: 2625
           TITLE OF INVENTION: PAX8-PPARGamma NUCLEIC ACID MOLECULES
TITLE OF INVENTION: AND POLYPEPTIDES AND USES THEREOF
FILE REFERENCE: BOOL/17.9(FBR/MAT
CURRENT APPLICATION WUMBER: US/09/765,111A
FRIOR APPLICATION NUMBER: US 60/177,109
FRIOR FILING DATE: 2000-01-20
FRIOR FILING DATE: 2000-01-20
FRIOR FILING DATE: 2000-01-20
FRIOR FILING DATE: 2000-01-20
FRIOR FILING DATE: 2000-08-14
NUMBER OF SEQ ID NOS: 47
SOFTWARE: FASTSEQ for Windows Version 3.0
SEQ ID NO 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 26, Application US/09765111A
Patent No. US20020106796A1
GENERAL INFORMATION:
APPLICANT: Fletcher, Jonathan A.
APPLICANT: Kroll, Todd G.
ITLE OF INVENTION: PAX8-PPARgamma NUCLEIC ACID MOLECULES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1150 CATGGTGGCAGAAATGACCATGGTTGACACAG 1181
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Best Local Similarity 96.9%
Matches 31, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; NAME/KEY: CDS
; LOCATION: (161)...(2596)
US-09-765-111A-22
                                                                                                                                                                                                                                                                                                                                                                          TYPE: DNA
ORGANISM: Homo Sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: DNA
ORGANISM: Homo Sapiens
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, LOCATION: (1)...(2625)
US-09-765-111A-5
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US-09-765-111A-26
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US-09-765-111A-5
                                                                                                                                                                                                                                                                                                                                                                                                                                 FEATURE:
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APPLICANT: Kroll, Todd G.

TITLE OF INVENTION: PAX8-PPARgamma NUCLEIC ACID MOLECULES
TITLE OF INVENTION: PAX8-PPARgamma NUCLEIC ACID MOLECULES
TITLE OF INVENTION: AND POLYPEPTIDES AND USES THEREOF
FILE REFERENCE: BO801/7195/ERF/MAT
CURRENT APPLICATION NUMBER: US/09/765,111A
CURRENT FILING DATE: 2001-01-18
PRIOR APPLICATION NUMBER: US 60/177,109
PRIOR FILING DATE: 2000-01-20
PRIOR FILING DATE: 2000-01-20
PRIOR FILING DATE: 2000-08-14
NUMBER OF SEQ ID NOS: 47
SOFTWARE: FastSEQ for Windows Version 3.0
LENGTH. 2334
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Patent No. US20020106796A1

GENERAL INFORMATION:
APPLICANT: Electher, Jonathan A.
APPLICANT: Evoll, Todd G.
TITLE OF INVENTION: PAX8-PPARgamma NUCLEIC ACID MOLECULES:
TITLE OF INVENTION: AND POLYBETIDES AND USES THEREOF;
FILE REFERENCE: B0801/7196/ERP/MAT

CURRENT APPLICATION NUMBER: US/09/765. 11A

CURRENT APPLICATION NUMBER: US 60/177,109

PRIOR FILING DATE: 2000-01-20

PRIOR FILING DATE: 2000-01-20

PRIOR FILING DATE: 2000-01-20

PRIOR FILING DATE: 2000-08-14

NUMBER OF SEQ ID DNOS: 47

SOFTWARE: FastSEQ for Windows Version 3.0
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Best Local Similarity 100.0%; Pred. No. 4.9e-08;
Matches 42; Conservative 0; Mismatches 0;
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US-09-765-111A-22
US-09-765-111A-22
Sequence 22, Application US/09765111A
Patent No. US20020106796A1
GENERAL INFORMATION:
APPLICANT: Fletcher, Jonathan A.
APPLICANT: Kroll, Todd G.
                                                                                                                                                                                                                                                                                                                                                                                              TYPE: DNA
ORGANISM: Homo Sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; NAME/KEY: CDS
; LOCATION: (1)...(2334)
US-09-765-111A-1
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ORGANISM: Homo Sapiens
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US-09-765-111A-11
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NAME/KEY: CDS
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                                                                                                                                                                        TITLE OF INVENTION: No. US20020150898Alel Mucleic Acids and
TITLE OF INVENTION: No. US20020150898Alel Mucleic Acids and
TITLE OF INVENTION: Polypeptides
TITLE OF INVENTION: Polypeptides
FILE REFERENCE: 91CIP2E
CURRENT APPLICATION NUMBER: US/09/816,828
CURRENT FILING DATE: 2001-03-22
PRIOR APPLICATION NUMBER: 09/770,160
PRIOR FILING DATE: 2001-01-26
PRIOR FILING DATE: 2000-04-18
NUMBER OF SEQ ID NOS: 18
SOFTWARE: PL_Genes Version 2.0
SEQ ID NO 8
LENGTH: 2260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Zhao, Oing A.
APPLICANT: Zhao, Oing A.
APPLICANT: Zhao, Oing A.
APPLICANT: Zhang, Jian-Rui
APPLICANT: Wang, Jian-Rui
APPLICANT: Wang, Jian-Rui
APPLICANT: Wang, Jian-Rui
APPLICANT: Drmanac, Radoje T.
TITLE OF INVENTION: No. US20020150898A1e1 Nucleic Acids and
TITLE OF INVENTION: Polypeptides
TITLE OF INVENTION: Polypeptides
TITLE OF INVENTION: Polypeptides
CURRENT APPLICATION NUMBER: US/09/816,828
CURRENT FILING DATE: 2001-03-22
PRIOR PILING DATE: 2001-01-26
PRIOR APPLICATION NUMBER: 09/770,160
PRIOR APPLICATION NUMBER: 09/552,929
PRIOR FILING DATE: 2000-04-18
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; Sequence 9, Application US/09816828
; Patent No. US20020150898A1
; EDERAL INPORMATION:
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SEQ ID NO 9
LENGTH: 2329
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Best Local Similarity 91.4
Matches 32; Conservative
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Goodrich, Ryle
Asundi, Vinod
                                 Xue, Aidong J.
Ma, Yunqing
Wang, Zhiwei
Zhao, Qing A.
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Xue, Aidong J.
Ma, Yunqing
Wang, Zhiwei
Zhao, Qing A.
                                                                                                                                 Zhang, Jie
Wang, Jian-Rui
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; NAME/KEY: CDS
; LOCATION: (1612)..(2142)
US-09-816-828-8
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; LOCATION: (1612)..(2211)
US-09-816-828-9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Tang, Y. Tom
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: DNA
ORGANISM: Homo sapiens
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ORGANISM: Homo sapiens
                                                                                                                                 APPLICANT:
APPLICANT:
                                                                                                       APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FEATURE:
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Patent No. US20020142981A1

GENERAL INFORMATION:

APPLICANT: USCALET T.

APPLICANT: Vockley, Joseph G.

APPLICANT: Scharf, Uwe

APPLICANT: Gene Logic, I.

ITILE OF INVENTION: Gene Expression Profiles in Liver Cancer;

FILE REFERENCE: 44921-5028-WO

CURRENT APPLICATION NUMBER: US 60/211,379

PRIOR PILING DATE: 2001-06-14

PRIOR PRILING DATE: 2000-06-14

PRIOR PRILING DATE: 2000-10-02

ABER OF SEQ ID NOS: 3950

LEWARE: PRICH OF SEQ ID NOS: 3950

LEWARE: LINE APPLICATION WINGER: US 60/237,054

PRIOR PLING DATE: 2000-10-02

ABER OF SEQ ID NOS: 3950

LEWARE: LINE APPLICATION VET: 2.1

SEQ ID NO 2212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             71.9%; Score 30.2; DB 10; Length 1811; 91.4%; Pred. No. 0.0031; live 0; Mismatches 3; Indels 0;
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; OTHER INFORMATION: Genbank Accession No. US20020142981A1 L40904
US-09-880-107-2212
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FILE OF INVENTION: AND POLYPEPTIDES AND USES THEREOF
FILE REFERENCE: B0801/7196/ERP/MAT
CURRENT APPLICATION NUMBER: US/09/765,111A
CURRENT FILING DATE: 2001-01-18
PRIOR APPLICATION NUMBER: US 60/17,109
PRIOR RILING DATE: 2000-00-120
PRIOR RILING DATE: 2000-00-14
PRIOR RILING DATE: 2000-00-14
NUMBER OF SEQ ID NOS: 47
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 26
JENGTH: 1811
TYPE: DMA
ORGANISM: HOMO Sapiens
FEATURE:
NAME/KEY: CDS
JOCATION: (173)...(1609)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  157 CGCCGTGGCCGCAAATGACCATGGTTGACACAG 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 157 CGCCGTGGCCGCAGAATGACCATGGTTGACACAG 191
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US-09-816-828-8/c
; Sequence 8, Application US/09816828
; Patent No. US20020150898A1
; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Zhou, Ping
; APPLICANT: Goodrich, Ryle
; APPLICANT: Asundi, Vinod
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 91.45
Matches 32; Conservative
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ORGANISM: Homo sapiens
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US-09-880-107-2212
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RESULT 12
US-09-765-111A-15
Sequence 15, Application US/09765111A
; Patent No. US20020106796A1
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Query Match
Best Local Similarity 78.9%
Matches 30; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches 23; Conservative
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NAME/KEY: CDS
LOCATION: (91)...(1608)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Homo Sapiens
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                                                                                                                                                                                                                                                                                               Sequence ) Application US/09765111A;
Sequence ) Application US/09765111A;
Patent No. US20020106796A1
GENERAL INFORMATION:
APPLICANT: Fletcher, Jonathan A.
APPLICANT: Froil, Todd G.
TITLE OF INVENTION: PAX8-PPARgamma NUCLEIC ACID MOLECULES
TITLE OF INVENTION: AND POLYPEPTIDES AND USES THEREOF
FILE REFERENCE: B0801/7196/ERP/MAT
CURRENT FILING DATE: 2001-01-18
PRIOR APPLICATION NUMBER: US/09/765,111A
PRIOR FILING DATE: 2000-01-20
PRIOR FILING DATE: 2000-01-20
PRIOR FILING DATE: 2000-01-8
NUMBER OF SEQ ID NOS: 47
SOFTWARE: FastSEQ for Windows Version 3.0
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GENERAL INFORMATION:
APPLICANT: Fletcher, Jonathan A.
APPLICANT: Fletcher, Jonathan A.
APPLICANT: Fletcher, Jonathan A.
TITLE OF INVENTION: PAXB-PPARGamma NUCLEIC ACID MOLECULES
TITLE OF INVENTION: PAXB-PARGamma NUCLEIC ACID MOLECULES
FILE REFERENCE: BO801/7196/ERP/MAT
CURRENT FILING DATE: 2000-01-20
PRIOR APPLICATION NUMBER: US 60/177,109
PRIOR APPLICATION NUMBER: US 60/225,079
PRIOR APPLICATION NUMBER: US 60/225,079
PRIOR FLING DATE: 2000-08-14
NUMBER OF SEQ ID NOS: 47
SOFTWARE: FASCEQ for Windows Version 3.0
                                                                        Indels
                        ch 71.9%; Score 30.2; DB 10; 1 Similarity 91.4%; Pred. No. 0.0033; 32; Conservative 0; Mismatches 3;
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                                                                                                                                                                         Db 1655 CGCCGCGCAGAAAGACCATGGTTGACACAG 1621
                                                                                                                              8 CCCCGTGGTGGCAGAATGACCATGGTTGACACAG 42
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: DNA
ORGANISM: Homo Sapièns
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TYPE: DNA
ORGANISM: Homo Sapiens
FEATURE:
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US-09-765-111A-3
                          Query Match
Best Local Similarity
Matches 32; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ) NAME/KEY: CDS
; LOCATION: (3)...(41)
US-09-765-111A-9
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LENGTH: 42
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Fatent No. US20020119499A1
GENERAL INCORMATION:
APPLICANT: TANABE SEIYARU CO. LTD.
APPLICANT: TANABE SEIYARU CO. LTD.
APPLICANT: TANIGUCHI, TOMOYASU
APPLICANT: TANIGUCHI CO. LTD.
ITILE OF INVENTION: ANTAGONIST TO PPAR
FILE OF INVENTION: ANTAGONIST TO PPAR
CURRENT APPLICATION NUMBER: US/10/109,886
CURRENT FILING DATE: 2000-20-40.1
PRIOR APPLICATION NUMBER: 09/514,247
PRIOR APPLICATION NUMBER: DOT/UD98/03734
PRIOR PLING DATE: 1998-08-24
PRIOR FILING DATE: 1998-08-24
PRIOR FILING DATE: 1998-08-24
PRIOR FILING DATE: 1998-08-24
PRIOR FILING DATE: 1998-08-24
SPROR PLING DATE: 1998-08-27
SOFTWARE: PALENTIN NUMBER: J99-108-27
SOFTWARE: PALENTIN VERSION 3.0
SOFTWARE: PALENTIN VERSION 3.0
SOFTWARE: PALENTIN VERSION 3.0
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                                                                     o;
      Length 2523;
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                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
APPLICANT: Fletcher, Jonathan A.
APPLICANT: Fletcher, Jonathan A.
APPLICANT: Fletcher, Jonathan A.
APPLICANT: Fletcher, Jonathan A.
TITLE OF INVENTION: PAX8 - PPARGamma NUCLEIC ACID MOLECULES
TITLE OF INVENTION: AND POLYPEPTIDES AND USES THEREOF
FILE REPRENCE: BORO1/196/ERP/MAT
CURRENT APPLICATION NUMBER: US 60/177,109
PRIOR FILING DATE: 2000-01-28
PRIOR APPLICATION NUMBER: US 60/177,109
PRIOR APPLICATION NUMBER: US 60/225,079
PRIOR FILING DATE: 2000-08-14
NUMBER OF SEQ ID NOS: 47
SOFTWARE: FRAELSEQ for Windows Version 3.0
                                                                     Indels
60.0%; Score 25.2; DB 10; 78.9%; Pred. No. 0.37; tive 0; Mismatches 8;
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LOCATION: (159)..(1679)
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US-10-109-886-5

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Search completed: January 22, 2003, 02:09:54 Job time : 30 secs
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; ...eDI NO. US2002017552A1
; GENERAL INFORMATION:
; APPLICANT: Jiang, Yuqiu
; APPLICANT: Jiang, Yuqiu
; APPLICANT: Gerrist, Heather
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF COLON CANCER
; FILE REFERENCE: 210121.57
; CURRENT APPLICATION NUMBER: US/09/878,178
; CURRENT FILING DATE: 2001-06-08
; NUMBER OF SEQ ID NOS: 2237
; SOFTWARE: FastSEQ for Windows Version 4.0
                                 Query Match 54.8%; Score 23; DB 12; Length 1679; Best Local Similarity 100.0%; Pred. No. 2.7; Matches 23; Conservative 0; Mismatches 0; Indels C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 52.4%; Score 22; DB 9; Length 343; Best Local Similarity 100.0%; Pred. No. 4.8; Matches 22; Conservative 0; Mismatches 0; Indels
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Best Local Similarity 100.0
Matches 22; Conservative
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ORGANISM: Homo sapiens
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TYPE: DNA
ORGANISM: Homo sapien
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BQ655082 NXRV090 A AL411958 T3 end of BF652561 276153 MA BJ493993 BJ493993

AW290590 NXNV031H1 BF609114 NXSI 040 AZ286381 RPCI-23-1 B92851 CIT-HSP-216

AZ084869 RPCT-23-3 BJ515912 BJ515912 BF742007 CM4-HB002 BF844064 MR2-HT104 BE865554 601677894

AA053612 2173f06.r AA012491 CTT-HSSP-2 AA14023 EST185P-3 BC569798 602590418 AV666708 AV666708 BC32333 602422963 BM790089 K.EST0069 BC288656 602385452 BM74097 601595318 BM744097 K.EST0017 BES88905 194571 BA AW954835 EST366905 BC367033 60142867 BC3686905 1044807 BC3686905 1044807 BC3686905 1044807 BC3686905 1044867

AA496551 zv38d01.s BE747612 601577470 BI523909 603051651 BQ25271 AGENCORFT AU137089 AU137089

BF680004 602154718 BG432259 602496557 BE742094 601575865 BE540092 601060887 BE748366 601572070 BG436329 602508773

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AL43579 903 bp mRNA linear EST 16-FEB-2001 AL543579 LTI NFL006 PL2 Homo sapiens CDNA clone CSODI006Y110 5 AL543579
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/db_xref="taxon:9606"
/db_xref="CS0D1006YI10"
/clone_lib="LTI NPL006_PL2"
/tissue_type="placenta"
/note="Vector: pCMVSPORT 6; Site_1: NotI; 1st strand cDNA
was primed with a NotI-oligo(dT) primer. Five prime end
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                                                                                                         AZ084869
BJ515912
BF742007
BF844064
BE86554
AA053612
AQ012491
AA314023
AG56978
BG565798
BG56708
            BF609114
AZ286381
B92851
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BG288656
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BM744007
BBS 8905
AW954835
BBS 67033
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BB 6348899
BB 73486551
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AL543579
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                                                                                    January 21, 2003, 23:02:45 ; Search time 1003.67 Seconds (without alignments) 677.725 Million cell updates/sec
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           GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
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71 CGCCGTGGCCGCAGAATGACCATGGTTGACACAG 105
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         cloned into the Not I and Eco RV sites of the pcNVSpORT 6
vector. Library was normalized. Library was constructed by
Life Technologies. Context: Feng liang life Technologies,
a division of Invitrogen 9800 Medical Center Drive
Rockville, Maryland 20850, USA Pax: (1) 301 610 8371
Email: filangelifetech.com URL:
http://fullnength.invitrogen.com.
a 228 c 220 g 205 t 1 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="Organ: pooled brain, lung, testis; Vector:
pCMV-SPORT6; Site 1: NotI; Site 2: ECGNV (destroyed); RNA
source anonymous pool of 6 male brains, age range 23-27; 1
male lung, age 27; and 1 male testis, age 69. Library is
oligo-dT primed and directionally cloned (ECGNV site is
destroyed upon cloning). Average insert size 1:8 kb,
insert size range 1-3 kb. Library is normalized and
enriched for full length clones and was constructed by C.
                                                                                                                                                                                                                                                                                              ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                               AGENCOURT 6707162 NIH_MGC_115 Homo sapiens cDNA clone IMAGE:5754203 BM922116
enriched, double-stranded cDNA was digested with Not I and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1141)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
Phttp://mage.llnl.gov
Plate: LLAM12791 row: d column: 12
High quality sequence stop: 105.
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National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
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                                                                                                                                                                                                                                            Score 30.2; DB 9; Length 903;
Pred. No. 0.19;
                                                                                                                                                                                                                                                                                         3; Indels
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                                                                                                                                                                                                                                                                                                                                                                     99 CGCCGTGGCCGCAGAATGACCATGGTTGACACAG 133
                                                                                                                                                                                                                                                                                                                                    8 CCCCGTGGTGGCAGAATGACCATGGTTGACACAG 42
                                                                                                                                                                                                                                                                                         0; Mismatches
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/db_xref="taxon:9606"
/clone="IMAGE:5754203"
/clone_lib="NIH_MGC_115"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
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1 Similarity 91.4%;
32; Conservative
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Best Local Similarity
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Best Local Similarity
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ORGANISM
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TITLE
JOURNAL
COMMENT
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BM922116
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KEYWORDS
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Gaps

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Indels

3,

8 CCCCGTGGTGGCAGAATGACCATGGTTGACACAG 42

Matches

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/note="Organ: pooled colon, kidney, stomach; Vector: pCMV-Sir 716; Site_1: Not1; Site_2: EcoRV (destroyed); RNA source alongwous pool of 3 colons, age 26 yo male, 49 yo female, 71 yo male colon; 46 yo male kidney, and pool of 2 stomachs, 62 yo male colon; 46 yo female. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.4 kb, insert size range 1-3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 03.3. Note: this is a NIH MGC Library."
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BM924484 11-MAR-2002 mRNA linear EST 12-MAR-2002 AGENCOURT_6767565 NIH_MGC_116 Home sapiens cDNA clone IMAGE:5760840
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RC5-NN1165-251100-024-H08 NN1165 Homo sapiens CDNA, mRNA sequence.
BF957583
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 526)
                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM12808 row: column: 01
High quality sequence start: 95
High quality sequence start: 95
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                  NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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Pred. No. 73;
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                                                                                                                                                                                                                                                                                                                                                                             Unpublished (1999)
Orditat: Robert Strausberg, Ph.D.
Email: cgapbs-remail nih gov
Tissue Procurement: Life Technologies, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /db xref="taxon:9606"
/clone="IMAGE:5760840"
/clone_lib="NIH_MGC_116"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Homo sapiens"
                                                                                                                                                                                                                                                                 Mammalia; Butheria; Primates;
1 (bases 1 to 1243)
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100.0%; Pre-
0; }
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                                                                                                               BM924484.1 GI:19374863
                                                       5', mRNA sequence.
BM924484
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Best Local Similarity
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/db Aref="lower adplets"
/db Aref="lower adplets"
/clone="IRAGE:517331"
/clone lib="UNH MGC 115"
/lab host="Thing lib="Index 115"
/lab host="Organ: pooled brain, lung, testis; Vector:
poww-sporfs, Site 1: Noti; Site 2: EcoRV (destroyed); RNA source anonymous pool of 6 male brains, age range 23-27; l male lung, age 27; and 1 male testis, age 69. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size is 8 kb, insert size range 1-3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 021. Note: this is a NIH MGC Library."
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Hordeum vulgare.

Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta, Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;

Triticaee; Hordeum.

(bases 1 to 700, N. Manhofs, A., Wise, R., Begum, D., Frisch, D. Yu. Y., Henry, D., Palmer, M., Rambo, T., Simmons, J., Choi, D. M., Fent, J.

NED, Oates, R. and Malin, D.

Development of a genetically and physically anchored EST resource for barley genomics: Morex drought-stressed seedling shoot cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EST 22-OCT-2001
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Unpublished (2001)
Unpublished (2001)
Unbec 19, 2000 this sequence version replaced gi:11892713.
Contact: Wing RA
Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Tel: 864 656 7288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HVSMED0006112f Hordeum vulgare seedling shoot EST 12:
HVSDNA0002 (Dehydration stress) Hordeum vulgare cDNA clone
HVSMED0006112f, mRNA sequence.
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  found through the 1.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Plate: LLAMI1436 row: m column: 16
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Pred. No. 1.6e+02;
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/organism="Homo sapiens"
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Total Mq bases = 482
Seg primer: AATTAACCCTAAAGGG
High quality sequence stop: 611.
                                                                              High quality sequence stop: 876.
Location/Qualifiers
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/clone="HVSMEb0006112f"
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SOURCE
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                                                                                                          FEATURES
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Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagal, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H., Brunstein, A., deolivedra, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
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                                                                                                                                                                                                                                                                                                                                                                                                                     Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.bx/scripts/gethtml2.pl?tl=RC5&t2=RC5-NN1165-251100-024-H08&t1=2000-11-25&t4=1)
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                                                                                                                                                                                                                                               Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                    Shotgun sequencing of the human transcriptome with ORF expressed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I M.A.G.E. Consortium (LINL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="NN1165"
/dev_stage="Adult"
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Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Seq primer: puc 18 forward
High quality sequence start: 52
High quality sequence stop: 523.
Location/Qualiffers
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BI820841.1 GI:15932391
                                                                                                                                                                                                                                                                                                                                                                              Tel: +55-11-2704922
                                                                                                                                                                                                                                                                                                                                                                                                        Fax: +55-11-2707001
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                                                                                                                                                                              sequence tags
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                                                                                                                          Simpson, A.J
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VERSION
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COMMENT
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BI820841
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/ciscue_type="xid"
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/cell_type="xid"
/dev_stage="Juvenile"
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/lab_bost="xid="labue"
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/l
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Pinus; Pinus.
1 (bases 1 to 514)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Pinus taeda"
/strain="Coastal plain loblolly pine from North Carolina"
/db_xref="taxon:3352"
/dlone="NxSI 040 E09"
/clone="NxSI 040 E09"
/clone="NxSI 040 E09"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sederoff, R . Mode Formation in the Pine Megagenome Molecular Basis of Wood Formation in the Pine Megagenome
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Pred. No. 2e+02;
0; Mismatches 11; Indels 0;
                                                                                                  53.3%; Score 22.4; DB 10; Length 463; 72.5%; Pred. No. 1.9e+02;
      17 others
                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                    102 GGCATATCCTGAGGTGGCAGTGAAGACCATGGCTCACATA 141
                                                                                                                                                                                                                            2 GACCTACCCCGTGGCAGAAATGACCATGGTTGACACA 41
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      127 t
                                                                                                                                                                  0; Mismatches
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Contact: Johnson, Arthur
North Carolina State University
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: ajohnson@unity.ncsu.edu
Seq primer: T3.
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   97 C
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Fax: 919 515 7801
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AZ286381
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                                                                                                                                                                            outliving in the dark at loow temperature on inter paper with water, nystain and cefotaxime in covered crystallization dishes. Five-day old seedlings were incubated at 90% RH for 24 hr. Shocts were then harvested, total RNA was prepared, poly(A) RNA was purified, one primary unamplified obbal library was made, 600000 pfu were primary unamplified cobal library was made, 600000 pfu were in vivo excised to give pbluescript SK(-) CDNA phagemids. These steps were performed in the TU Close laboratory at the University Genomics Institute (UGGI) (Begum, Palmer, Frisch, Atkins and Wing). Plasmid DNA perparations, DNA sequencing and sequence analysis were performed at CUGI (Wing, Yu, Frisch, Henry, Simmons, Oates, Rambo, Main). The sequence has been trimmed to remove vector sequence and contains a minimum of 100 bases of phred value 20 or above. For more details on library preparation and
                                                                                           /note="Wector: lambdaZAP; Site 1: EcoR1; Site 2: Xho1; Seeds were surface sterilized then germinated_under axenic conditions in the dark at room temperature on filter paper
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/note="Vector: BlueScript SK, Site 1: BCo RI, The
sequences contain a 'cDNA adapter' between the EcoRI site
and the start of the EST. The adapter sequence is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Pinus; Pinus.
1 (bases 1 to 463)
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NXNV031H10F Nsf Xylem Normal wood Vertical Pinus taeda CDNA clone
NXNV031H10 5', mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             http://www.genome.clemson.edu/projects/barley. To order
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               this clone see http://www.genome.clemson.edu/orders Al
see Close TJ, Wing K, Kleinhofs A, Wise R (2001)
Genetically and physically anchored BST resources for
barley genomics. Barley Genetics Newsletter 31:29-30.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (http://wheat.pw.usda.gov/ggpages/Lgn/31/cover.ltml)"
212 c 202 g 139 t
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Contact: Johnson, Arthur
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0
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HVcDNA0002 (Dehydration stress)"
                                     tissue_type="Seedling shoot"
lab host="TJC121"
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Tel: 919 515 7800
Fax: 919 515 7801
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/clone="NXNV031H10"
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KEYWORDS
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648 bp mRNA linear EST 15-JUL-2002
NXRV090 A07_F NXRV (Nsf Xylem Root wood Vertical) Pinus taeda cDNA
clone NXRV090_A07 5', mRNA sequence.
BQ655082
                                                                                                                              Conteact: Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0200
Email: mdadams@tigr.org
Clones are available from Research Genetics (info@resgen.com). BAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Coniferopsida, Coniferales, Pinaceae, Pinus, Pinus.
1 (bases 1 to 648)
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| Strain="Coastal plain loblolly pine from North Carolina" |
| Ab xref="taxon:3352" |
| Clone="NXKV090 A07" |
| Clone="NXKV090 A07" |
| Clone="NXKV090 A07" |
| Clone lib="NXKV (Nsf Xylem" Root wood Vertical)" |
| Clone lib="NXKV (lem Xylem" |
| Cell type="Root (primary)" |
| Cell type="Root (primary)" |
| Absorptional" |
| Cell type="Transitional" |
                                                                                                                                                                                                                                                                                                                        end search page:
http://www.ligr.org/tdb/humgen/bac_end_search/bac_end_search.html
Seg primer: M13 Reverse
Class: BAC ends.
                                        Use of a random BAC End Sequence Database for Sequence-Ready Map Building (1998)
Unpublished (1998)
Other_GSSs: CIT-HSP-2164L16.TF
Golden, K., Berry, K., Granger, D., Suh, E., Wible, C., Shizuya, H.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /db_xref="taxon:9606"
/clone="2164116"
/clone=lb="clT-HSP"
/sex="Male"
/cell_type="Sperm"
/note="Vector: pBeloBAC11; Site_1: HindIII; Site_2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sederoff.R. Molecular Basis of Wood Formation in the Pine Megagenome Unpublished (2004) Arthur North Carolina State University
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81.2%; Pred. No. 2.1e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Homo sapiens"
/db_xref="GDB:7100882"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Tel: 919 515 7800
Fax: 919 515 7801
Email: ajohnson@unity.ncsu.edu
                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
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                     Simon, M. and Venter, J
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Pinus taeda
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BQ655082
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Zhao, S., Nierman, W., Feldblyum, T., Malek, J., Shatsman, S., Akinret
Zhao, S., Nierman, W., Mcgann, S., Tsegaye, G., Geer, K., Krol, M., de Jong, P.
and Fraser, C.M.
Mouse BAC End Sequences from Library RPCI-23
Unpublished (1999)
Other GSSs: RPCI-23-155J16.TV
Contact: Shaying Zhao
Contact: Shaying Zhao
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      with a combination of EcoRI and EcoRI Methylase. Size selected DNA was cloned into the PBACe3.6 vector at the EcoRI sites. The ligation products were transformed into PH10B electrocompetent cells (BRL Life Technologies).
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CIT-HSP-2164L16.TR CIT-HSP Homo sapiens genomic clone 2164L16, DNA
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 544)
Adams,M.D., Rounsley,S.D., Zhao,S., Field,C.E., Bass,S., Linher,K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: szhaogeigr.org
Clones are derived from the mouse BAC library RPCI-23. For BAC
Library availability, please contact Pieter de Jong
(pieter@dejong.med.buffalo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/orderingframe.htm)
or from Resea ch Genetics (info@resgen.com). BAC end page:
http://www.tigr.org/db/bac_ends/mouse/bac_end_intro.html
Seq primer: SP6
Class: BAC ends.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="Organ: Kidney/Brain, Vector: pBACe3.6; Site 1: EcoRI; Site_2: EcoRI; Female C57BL/6J mouse kidney and/or brain genomic DNA was isolated and partially digested with a combination of EcoRI and EcoRI Methylase. Size
                                                                                                        Mus musculus
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalla, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
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                                                                                                                                                                                                                                                                                                                                                                                                             USA
                                                                                                                                                                                                                                                                                                                                                       Department of Bukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850,
Fax: 301 838 0206
Fax: 301 838 0206
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Mus musculus"
/strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /db_xref="taxon:10090"
/clone="RPCI-23-155J16"
/clone_lib="RPCI-23"
/sex="Female"
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                                        AZ286381.1 GI:9528090
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'lab host≈"XL1-Blue"

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Fis GSS is part of a random genomic sequencing program of thirteen yeast species: Saccharomyces bayanus var. uvarum, Saccharomyces servazzii, Zygosaccharomyces rouxii, Saccharomyces servazzii, Zygosaccharomyces rouxii, Saccharomyces servazzii, Zygosaccharomyces rouxii, Saccharomyces kluyveri, Kluyveromyces thermotolerans, Kluyveromyces lactis var. lactis, Kluyveromyces thermotolerans, Kluyveromyces angusta, Debaryomyces hansenii var. hansenii, Pichia sorbitophila, Candida tropicalis and Yarrowia lipolytica. Genomic inserts of 3 to ke were prepared and both extremities were sequenced. See keywords for description of this sequence and for the sequence of the other extremity of this insert.
/note="Vector: pBlueScript SK-; Site 1: Eco RI; Site 2: XhoI; The library is from primary xylem scraped from the roots of a twelve year old tree in the transitional phase from juvenile wood to mature wood production. NOTE: The sequences contain a 'cDNA adapter' between the EcoRI site and the start of the ESI. The adaptersequence is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            991 bp DNA linear GSS 05-JUL-2001
T3 end of clone AW0AA014D09 of library AW0AA from strain CLIB 89 of
Yarrowia lipolytica, genomic survey sequence.
AL411958
AL411958.1 GI:12181936
GSS.
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Direct Submission

Submitted (07-SEP-2000) Genoscope - Centre National de Sequencage,
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Bolotin-Fukuhara,M., Bon,E., Brottier,P., Casaregola,S.,
de-Montigny,J., Duljon,B., Durrens,P., Lepingle,A., Llorente,B.,
Malpertuy,A., Neweglise,C., Ozier-Kalogeropoulos,O., Potier,S.,
Saurin,W., Tekaia,F., Toffano-Nioche,C., Wesolowski-Louvel,M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Yarrowia lipolytica
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
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FEBS Lett. 487 (1), 3-12 (2000)
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/db_xref="taxon:4952"
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Wincker, P. and Weissenbach, J.
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1 (bases 1 to 490)
Smith, T.P. L., Grosse, W. M., Freking, B. A., Roberts, A. J., Stone, R. T., Casas, E., Wray, J. E., White, J., Cho, J., Fahrenkrug, S. C., Bennett, G.L., Heaton, M. P., Laegreid, W. W., Rohrer, G. A., Chitko-McKown, C. G., Fertea, G., Holt, I., Karamycheva, S., Liang, F., Quackenbush, J. and Keele, J. W.
                                                                                                                                                                                                                                                                                                                                                                                                                                       EST 25-APR-206.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="Vector: pCMV SPORT6; Site_1: Not1; Site_2: Sal1; Library made from pooled tissue from marrow, alveolar macrophage, ovary, fetal semitendonosus muscle, and fetal longissimus muscle."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Single pass sequencing. Bases called and alt trimmed with phred v0.980904.e. Vector identified by cross_match with the -minscore and -minmatch 12 options.

PCR PRIMER'S

FORWARD: AGGAAACAGCTATGACCAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence evaluation of four pooled-tissue normalized bovine cDNA libraries and construction of a gene index for cattle Genome Res. 11 (4), 626-630 (2001)
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                                                                                                                                                          Length 991;
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                                                                                                                                                                                                                                                                                                                                                                                                                               BF652561 1inear 276153 MARC 3BOV Bos taurus cDNA 5', mRNA sequence.
                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       USDA, ARS, US Meat Animal Research Center PO Box 166, Clay Center, NE 68933-0166, USA e1s. 402 762 4366
Fax: 402 762 4390
Email: smith@email.marc.usda.gov
                                                                                                                                                          17;
                                                                                                                                                                                                                                                                                               764 ACTAAACCTGTAGTGGCAGAAGTTACCATGGCTGTAACTG 803
                                                                                                                                                                                                                                                       3 ACCTACCCCGTGGTGGCAGAATGACCATGGTTGACACAG 42
                                                                                                                                                       Score 22.4; DB 17
Pred. No. 2.9e+02;
0; Mismatches 11
                                                                             275 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /db_xref="taxon:9913"
/clone lib="MARC 3BOV"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BACKWARD: GTTTTCCCAGTCACGACG
Plate: 66 row: K column: 2
Seq primer: ATTTAGGTGACACTATAG.
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/lab_host="DH10B"
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/clone="AWOAAO14D09"
/clone_lib="AWOAA"
/note="end : T3"
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                                                                          258 g
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BF652561.1 GI:11917693
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72.5%;
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Search completed: January 22, 2003, 00:39:33 Job time : 1006.67 secs
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                                                                                                                                                                                         source
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ORIGIN
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                                                                                                                                                                 FEATURES
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                                      BJ493993 MF01FSA CDNA Oryzias latipes CDNA clone MF01FSA035D13 5',
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Zhao, S., Nierman, W., Feldblyum, T., Malek, J., Shatsman, S., Akinret, B., Levins, M., Mcgann, S., Tsegaye, G., Geer, K., Krol, M., de Jong, P. and Fraser, C.M.
                                                                                                                                                                                   Oryzias latipes
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygi; Neopterygi; Teleostei; Euteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Atherinomorpha;
Beloniformes; Adrianichthyidae; Oryzinae; Oryzias.
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
1 (bases 1 to 569)
                                                                                                                                                                                                                                                                                                         Kohara, Y., Shin-i, T., Kimura, T., Narita, T., Jindo, T. and Takeda, H. Medaka EST Project in Takeda's lab
Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Shaying Zhao
Department of Bukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
191: 301 838 0200
Fax: 301 838 0208
Email: szhao@tigr.org
                                                                                                                                                                                                                                                                                                                                                                                                                                1111 Yata, Mishima, Shizuoka 411-8540, Japan
Tel: 81-559-81-6856
Fax: 81-559-81-6855
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Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /sex="mixture of female and male"
                                                                                                                                                                                                                                                                                                                                                                        Contact: Tadasu Shin-i
Center For Genetic Resource Information
National Institute of Genetics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                456 ccaceeeeeeeaaraeceaccarearreacacae 490
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    8 CCCCGTGGTGGCAGAATGACCATGGTTGACACAG 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             organism="Oryzias latipes"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /strain="d-rR"
/db_xref="taxon:8090"
/clone="MF01FSA035D13"
/clone_lib="MF01FSA cDNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: tshini@genes.nig.ac.jp.
Location/Qualifiers
1. .558
                                                                                                                      BJ493993.1 GI:22145919
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Best Local Similarity 77.1%;
Matches 27; Conservative (
                                                                                                                                                                                                                                                                                            (bases 1 to 558)
                                                                                                                                                                 Japanese medaka.
                                                                                 mRNA sequence.
BJ493993
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                                                            DEFINITION
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AZ084869
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JOURNAL
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selected DNA was cloned into the pBACe3.6 vector at the BcoR sites. The ligation products were transformed into DH10B electrocompetent cells (BRL Life Technologies).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /sex="Female"
/lab_host="DH10B"
/lab_host="DH10B"
/note="Organ: Kidney/Brain; Vector: pBACe3.6; Site_1:
EcoR1; Site_2: EcoR1; Female C57BL/6J mouse kidney and/or
brain genomic DNA was isolated and partially digested
with a combination of EcoR1 and EcoR1 Methylase. Size
Clones are derived from the mouse BAC library RPCI-23. For BAC library availability, please contact Pieter de Jong (pieterédéjong med.buffalo.edu). Clones may be purchased from BACPAC Resources (http://bacpac.med.buffalo.edu/orderingframe.htm) or from Resea ch Genetics (info@resgen.com). BAC end page: http://www.tigr.org/tdb/bac_ends/mouse/bac_end_intro.html Plate: 35 row: K column: 15 Seg primer: T7 Class: BAC ends.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ch 52.9%; Score 22.2; DB 17; Length 569; 1 Similarity 77.1%; Pred. No. 2.5e+02; 27; Conservative 0; Mismatches 8: Indels n
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          152 GACCTICCACGGGGGGGGGAAAAGAACTIGGGTG 186
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    .569
    organism="Mus musculus"

                                                                                                                                                                                                                                                                                                                                                                                                                                                      /db_xref="taxon:10090"
/clone="RPCI-23-35K15"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /clone_lib="RPCI-23"
                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                      'strain="C57BL/6J"
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January 21, 2003, 23:02:20; Search time 775.333 Seconds (without alignments) 1576.506 Million cell updates/sec
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42
1 cgggccaggccctcctctca.....aatgaccatggttgacacag 42
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GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                            number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                2054640 segs, 14551402878 residues
                                                                                                                                                                                                                                                                                                                                                                       Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                       OM nucleic - nucleic search, using sw model
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Gapop 10.0 , Gapext 1.0
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Perfect score:
Sequence:
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Searched:

Run on:

Database :

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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

ription	AB005521 Homo sapi	347	.26 Homo	HOMO H	L40904 Homo sapien	AX409565 Seguence	AR139020 Sequence	AY048699 Macaca fa	AC103039 Rattus no	AC112596 Rattus no	AC004387 Homo sapi	AL672032 Human DNA	Y12419 B.taurus mR	AC121976 Mus muscu	AC027797 Homo sapi	AC087737 Homo sapi	AC025919 Homo sapi	ALS91003 Mouse DNA	AC025581 Mus muscu x93592 C canie bay	X9595 M.musculus	X83591 C.canis Pax	AC099634 Mus muscu	AC016683 Homo sapi	AL/32528 Mus muscu U63415 Human perox	AR121467 Sequence	U79012 Human ligan	AR203332 Sequence	D83233 Homo sapien	ALS12883 Human DNA		AC034116 Mus muscu	AC025356 Homo sapi	Z97832 Human DNA s	244	1962	C010906	71 Lemur ca	ξ.
SUMMARII	AB0055181	AC090947	AC027126	AC009471 HQDDARGAM	HUMPPARGB	AX409565	AR139020	AY048699	AC103039	AC112596	AC004387	AL672032	BIPPARGI	AC121976	AC027797	AC087737	AC025919	0 ALS91003	ACUZSSMI	0 MMPAX89	CCPAX8A	AC099634	AC016683	AL/32528 HSU63415	AR121467	HSU79012	AR203332	HUMPPARG	ALS12883	ACC33003	AC034116	AC025356	HS329A5	924	6	C01090	AC1239	3459
ery tch Length Di	67.6 416 9	166043	185608	172445	1808	1811	1844	2063	135011	182241	206156	209317	1/11 4	173755 2	173935	187088	188439 9	221647 1	1242	1361 1	1380	179150	179937	1518	1608	1608	1679	1679	104314	199763	200262	73615	117026	129155	143749	208571	221640 2	1128 1
ore	28.4		α,	. د	9 7 7 8	56	N	24.2										23.4	23.4 2.5	23.2	23.2	23.2	23.0	23.23	23	23	23	233	5.6	2,5	23	N	22.8	N	N I	N ·	N.	N
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## ALIGNMENTS

RESULT 1	
AB00552181	
LOCUS	AB005521S1 416 bp DNA linear PRI 14-APR-2000
DEFINITION	Homo sapiens ppar gamma gene for peroxisome proliferator
	activated-receptor gamma, exon 1.
ACCESSION	AB005521
VERSION	AB005521.1 GI:2605490
KEYWORDS	ppar gamma, ppar gamma common exonl; peroxisome proliferator
	activated-receptor gamma.
SEGMENT	1 of 6
SOURCE	Homo sapiens placenta DNA.
ORGANISM	Homo sapiens
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
	Mammaila; burneria; Frimares; Cararrnin; Hominidae; Homo.
REFERENCE	T.

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Direct Submission
Submitted (13-AUG-2001) Human Genomic Center, Institute of
Genetics, Chinese Academy of Sciences, Datun Road, Beijing, Beijing
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2 (bases 1 to 166043)
Wu.C., Bao.Q., Bao.W., Bian.X., Cao.T., Chen.C., Chen.J.,
Ding.H., Dong.W., Fan.H., Feng.X., Gong.J., Guan.Q., Gu.X., Guo.D.,
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Homo sapiens chromosome 3 clone RP11-30G23 map 3p, complete
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequencing vector: pUC18; 100% of reads
Chemistry: Dye-terminator: ET 55% of reads
Chemistry: Dye-terminator: ET 55% of reads
Assembly program: Phrap; version 0.990329
Consensus quality: 586 bases at least Q40
Consensus quality: 1154 bases at least Q30
Consensus quality: 1154 bases at least Q20
Insert size: 1198; sum-of-contigs
Quality coverage: 1.48x in Q20 bases;sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              67.6%; Score 28.4; DB 9; Length 135667; 96.7%; Pred. No. 0.76; 1.1ve 0; Mismatches 1; Indels 0;
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Center project Name:1% project
Center clone name: RP11-167M22
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                                                                                                                                                                                                                                                                         Center code.Beijing
Website:http://hgc.igtp.ac.on
http://www.genomics.org.cn
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/map="3p"
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AC090947.1 GI:13384351
                                                                                                                                                                                                                                                                                                                                                                                          Contact:hgc@igtp.ac.cn
                                                                                                                                                                                                                                      Center:Beijing Center
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               lu, J. and Yang, H.
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Yu,J. and Yang,H.
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Butaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Butaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.

Bao,J., Bao,Q., Bao,W., Bian,X., Cao,T., Chen,C., Chen,J., Guo,D., Guo,D., Guo,D., Guo,D., Guo,D., Guo,D., Cao,M., Li,C., Li,C.,
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Bao, J., Bao, W., Bian, X., Cao, T., Chen, C., Chen, J., Ding, H., Dong, W., Fan, H., Feng, X., Gong, J., Guan, Q., Gu, X., Guo, D., Guo, Z., He, L., Hu, S., Huang, F., Jin, Y., Kang, W., Li, C., Li, C., Li, F., Li, F., Li, Y., Liu, Y., Liu, W., Liu, W., Liu, B., Liu, Y., Liu, Y., Liu, W., Liu, W., Liu, W., Liu, W., Liu, W., Sung, Y., Sung, L., Song, S., Sun, M., Sun, W., Sun, Y., Tan, X., Tao, R., Wang, H., Wang, J., Wang, J., Wang, L., Wang, L., Wang, K., Wang, Y., Wang, J., Xie, F., Xuan, Z., Xue, Y., Yan, C., Yang, X., Wang, X., Zeng, Y., Zhang, H., Zhang, H., Zhang, M., Zhang, M., Zhang, X., Zhang, Y., Zhang, X., Zhang, Y., Zhang, X., Zhang, Y., Zh
                                                                                                                                                                                                                                                                                                    Direct Submission
Submitted (03-JUL-1997) Hideki Okazawa, Kobe University School of Medicine, 2nd Department of Internal Medicine, 7-5-1 Kusunoki-cho chuo-ku, Kobe 650, Japan (E-mail:okazawa@med.kobe-u.ac.jp, Tel:81-78-341-7451, Fax:81-78-382-2080)
Okazawa, H., Mori, H., Tamori, Y., Araki, S., Niki, T., Masugi, J., Kawanishi, M., Kubota, T., Sinoda, H. and Kasuga, M.
No coding mutations are detected in the peroxisome proliferator-activated receptor- gene in Japanese patients with lipoatrophic diabetes
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Homo sapiens chromosome 3 clone RP11-167M22 map 3p, complete
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Best Local Similarity 96.7%; Pred. No. 1.3;
Matches 29; Conservative 0; Mismatches 1;
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/tissue_type="placenta"
<115..340
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                                                                                                                                                                                       Diabetes (1997) In press 2 (bases 1 to 416)
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                                                                                                                                                                                                                                                                     Okazawa, H
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Yang, X.,

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Contact: hgc@igtp.ac.cn
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Guo, Z., He, L., Hu, S., Huang, F., Jin, Y., Kang, N., Li, C., Li, C., Li, C., Li, C., Li, C., Li, G., Gi, G., Gi, X., Song, L., Song, S., Sun, M., Sun, Y., Tan, X., Tao, R., Wang, H., Wang, L., Wang, R., Wang, H., Wang, X., Wang, Y., Wang, Y., Wang, X., Wang, X., Wang, Y., Wu, D., Xie, F., Xuan, Z., Xue, Y., Yan, C., Yang, X., Yu, B., Zeng, Y., Zhang, H., Zhang, H., Zhang, H., Zhang, M., Zhang, M., Di, R., C., Yang, X., Zhang, M., Zhang, M., Zhang, M., Zhang, M., Zhang, Y., Zhang, Y., Zhang, X., Zhang, M., Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                         Submitted (20-MAR-2001) Human Genomic Center, Institute of Genetics, Chinese Academy of Sciences, Datun Road, Beijing, Beijing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ..
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(Dassa: 1 to 188568)

Wu, O., Bao, J., Bao, W., Bian, X., Cao, T., Chen, C., Chen, J., Ding, H., Dong, M., Pan, H., Peng, X., Gong, J., Guan, Q., Gu, X., Guo, D., Guo, Z., He, L., Hu, S., Huang, F., Jin, Y., Kang, N., Li, C., Li, C., Li, C., Li, C., Li, T., Li, W., Li, M., Li, W., Li, Y., Li, W., Li, W., Li, Y., Li, W., Li, W., Li, Y., Li, W., Li, W., Sun, Y., Tan, X., Tao, R., Vang, H., Wang, J., Wang, L., Wang, L., Wang, L., Wang, L., Wang, R., Wang, R., Wang, X., Wang, Y., Wang, R., Wang, X., Wang, Y., Wang, X., Wang, Y., Wang, X., Wang, X.,
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Homo sapiens chromosome 3 clone RP11-586C12 map 3p, complete
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Quality coverage: 2.80x in Q20 bases;sum-of-contigs
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Sequencing vector: pUC18; 100% of reads
Chemistry: Dye-terminator: ET 55% of reads
Assembly program: Phrap; version 0.990329
Consensus quality: 499 bases at least Q40
Consensus quality: 605 bases at least Q30
Consensus quality: 674 bases at least Q30
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/db_xref="taxon:9606"
/chromosome="3"
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Center clone name: RP11-30G23
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Website:http://hgc.igtp.ac.cn
http://www.genomics.org.cn
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AC027126.4 GI:13236635
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Center:Beijing Center
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Augustano Direct Submission
Submitted (28-MAR-2000) Human Genomic Center, Institute of Genetics, Clinese Academy of Sciences, Datun Road, Beijing, Beijing 100101, P.R.China
100101, P.R.China
1 (bases 1 to 185608)
SS Wu,Q., Bao,W., Bian,X., Cao,T., Chen,C., Chen,J., Ding,H., Dong,W., Fan,H., Feng,X., Gong,J., Guan,Q., Gu,X., Guo,D., Guo,Z., He,L., Li,G., Li,J., Li,S., Li,T., Li,G., Li,J., Li,S., Li,T., Li,S., Li,
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Wang,X., Wang,Y., Wu,D., Xie,F., Xuan,Z., Xue,Y., Yan,C., Yang,X., Yu,B., Zeng,Y., Zhang,G., Zhang,H., Zhang,L., Zhang,M., Zhang,X., Zhang,X., Zhang,X., Zhang,Y., Zhang,Y., Zhang,Y., Zhang,Y., Zhang,Y., Zhu,B., Zhu,N., Yu,J. and Yang,H.
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96.7%; Pred. No. 0.74;
live 0; Mismatches 1;
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http://www.genomics.org.cn
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the RPCI-11 human BAC library was made from the blood of one male

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University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
6 (bases 1 to 172445)
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Submitted (24-AUG-1999) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (23-MAR-2001) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St. Louis,
                                      PRI 07-NOV-2001
                                                                                                                                                                                       Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (07-NOV-2001) Department of Genetics, Washington University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, on Mar 23, 2001 this sequence version replaced gi:9838098.
                        AC009471 172445 bp DNA linear PRI 07-W
Homo sapiens BAC clone RPll-168K7 from 2, complete sequence.
AC009471
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Direct Submission
Submitted (09-AUG-2001) Department of Genetics, Mashington
                                                                                                                                                                                                                                                                                                                                                                                  Scott, K., Kyung, K., Maupin, R., LaPlant, Y. and Reitz, L. The sequence of Homo sapiens BAC clone RPI1-168K7
                                                                                                                                                                                                                                                                             Toward a complete human genome sequence
Genome Res. 8 (11), 1097-1108 (1998)
                                                                                                                                                                                                                               1 (bases 1 to 172445)
Sulston, J.E. and Waterston, R.
                                                                                                 AC009471.5 GI:13435274
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5 (bases 1 to 172445)
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Waterston, R.H.
                                                                                                                                                                                                                                                                                                                                                                (bases 1 to 172445)
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Direct Submission
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                                                                                                                                                                     Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                             Unpublished
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                                                          DEFINITION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Center: Washington University Genome Sequencing Center
Center code: WUGSC
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Contact: sapiens@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Center project name: H_NH0168K07
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Mapping information for this clone was provided by Dr. John D. McPherson, Department of Genetics, Washington University, St. Louis MO. For additional information about the map position of this sequence, see http://genome.wustl.edu/gsc

SOURCE INFORMATION:

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donor, as described by Osoegawa, K., Woon, P.Y., Zhao, B., Frengen, E., Tareno, M., Catanese, J.J. and de Jong, P.J. (1998) An improved approach for construction of bacterial artificial chromosome libraries. Genomics 51:1-8. The clone may be obtained either from Research Genetics, Inc. (http://www.resgen.com) or Pieter de Jong and coworkers at the Roswell Park Cancer Institute
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EST AI819855 (NID:95438934) wj45g03.x1"
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                                                                                                                                                                                                                                                                                                                                    The sequence RP11-168K7 from base position 72908 to 74615 cannot be
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                                                                                                                                                                                                                                                                                                                                                                 The tandem size is believed to
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EST T59958 (NID:g661795) yc01h05.s1"
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                                                                                                                                                                                                                                                  Actual start of this clone is at base position 1 of RP11-168K7; actual end is at base position 172445 of RP11-168K7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           base position 120454 to 120643 for which the exact length is unknown. Assembly of the database is consistent with digest
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EST BF342851 (NID:g11289878)"
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be in agreement with digest information.
                                                                                                                                                                                           VECTOR: PARCE3.6
NEIGHBORING SEQUENCE INFORMATION:
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                                                                                                                                                                   (http://bacpac.med.buffalo.edu)
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/chromosome="2"
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1. .858
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ISTPHYEDIPFTRTDPVVADYXYDLKLQEYQSAIKVEPASPPYYSEKTQLYNKPHEEP
SNSLMAIECRVCGDKASGFHYGVHACEGCKGFFRRTIRLKLIYDRCDLNCRIHKKSRN
KCQYCRFQKCLAVGMSHNAIRFGRMPQAEKEKLLAEISSDIDQLNPESADLRALAKHL
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DGVLISGGCGFWTREPLKSLRKPRODFWEPKFEFAVKFNLLELDDSDLAIFIAU
GDRPGLLNVRPIEDIQDNLLQALELQLKLNHPESSQLFAKLLQKTDLRQIVTEHVQL
LQVYKKTETDMSHHPLLQEIYKDLY"

4 14 c 397 g 425 t
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VAIRIFQGCQFRSVBAVQEITEYAKSIPGFVNLDLANDQVTLLKYGVHEIIYTMLASLM
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LSGDRPGLLNVKPIEDIQDNLLQALELQLKLNHPESSQLFAKLLQKMTDLRQIVTEHV
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SLMAI ECRVCGDKASGFHYGVHACEGCKGFFRRTI RLKLI YDRCDLNCR I HKKSRNKC
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                                                                                                                                                               activated by inducers of adipogenesis, including thiazolidinedione
                                                        Craniata, Vertebrata, Buteleostomi,
Catarrhini, Hominidae, Homo.
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/product="peroxisome proliferator activated receptor
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/product="peroxisome proliferator activated receptor
                                                                           Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. I (bases 1 to 1767).
Lambe, K.G. and Tugwood, J.D.
A human peroxisome-proliferator-activated receptor-gamma is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .,
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peroxisome proliferator-activated receptor gamma
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/db_xref="GI:1490314"
/db_xref="SNISS-PROT:P37231"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                'db_xref="GI:1490313"
'db_xref="SWISS-PROT:P37231"
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109. .1536
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96305359
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /tissue type="placenta"
/clone lib="lambda ZAP II"
103. .1536
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        protein_id="CAA62152.1"
                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="CL15-2a-2"
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               Ĥomo sapiens.
Homo sapiens
Bukaryota; Metazoa; Chordata;
                                                                                                                                                                                                                                                                   2 (bases 1 to 1766)
Lambe, K.G.
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                                                                                                                                                                                                                                                                                                            Direct Submission
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Best Local Similarity
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HUMPPARGE
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                 EST A1347836 (NID:g4085042) gp03a08.x1"
                                                                                                                                                                                                                                                                 EST AA910154 (NID:g3049444) od92h01.sl"
                                                                                                                                                                                                                                                                                                                                                                                          (NID:92563631) ng85c10.s1"
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                                                        EST AA188866 (NID:g1775893) zp77e05.rl"
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                                                                                                                                     EST H80249 (NID:g1058338) yu87g12.rl"
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                                                                                               EST AU134393 (NID:g10994932)"
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Pred. No. 3.9;
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/note="similar to
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2812. .2849
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X90563.1 GI:1480099
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Mammalla, Butheria, Primates, Catarrhini, Hominidae, Homo.
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Greene, M.B. and Blumberg, B.
Human peroxisome proliferator activated receptor gamma:
compositions and methods
Patent: 18 6 2008 102-A 1 13-MAR-2001;
Location/Qualifiers
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85.3%; Pred. No. 10;
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                                                                                                                                                                            158 GCCGTGGCCGCAGAATGACCATGGTTGACACAG 191
                                                                                                                                                                                                                                                                                    AX409565 1811 bp Di Sequence 2212 from Patent WO0229103.
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AR139020
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Homo sapiens"
/db_xref="taxon:9606"
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433 c 421 g
                    422 g
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KCOVCRFCKCLAVGNSHNAIRFGRHWOPAEREKLAETSSDIDGLNBFSADLRALAKHI.
YDSYIKSFPLTKAKRALILTGKTTDKSFFYYYDMSLAMGGEDKIKEKHITPLODGOSKE
VISYIKSFPLTKAKRALILTGKTTDKSFFYYYDMSLAMGGEDKIKEKHITPLODGOSKE
VISTRIFGQCCFRSVEAVOEITEFYAKSIPGFWNLDLNDQVTLLKYGVHEIIYTMLASLM
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LSGBREGLLNVKPIEDDONLLOALELQLKLNHPESSQLFAKLLQKNTDLRQIVTEHV
QLLQVIKKTETDMSLHPLLQEIYKDLY"
                PRI 26-DEC-2001
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                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1808)
                                                                                                                                                                                                                      Greene, M.E., Blumberg, B., McBride, O.W., Yi, H.F., Kronquist, K., Kwan, K., Hsieh, L., Greene, G. and Nimer, S.D.
Isolation of the human peroxisome proliferator activated receptor gamma cDNA: expression in hematopoietic cells and chromosomal
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Submitted (26-DEC-2001) University of Chicago, Chicago, IL 60637,
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Homo sapiens peroxisome proliferator activated receptor gamma traces mana, complete cds.
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Greene, M.E., Blumberg, B., McBride, O.W., Yi, H.F., Kronguist, K.,
Kwan, K., Hsieh, L., Greene, G. and Nimer, S.D.
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On Dec 26, 2001 this sequenc: version replaced gi:722619.
Location/Qualifiers
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/dev_stage="adult"
1. .1808
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173, .1606
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/chromosome="3"
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6"
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FIAVIILSGDRPGLLNVKPIEDIQDNLLQALELQLKLNHPESSQLFAKLLQKWTDLRQ
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QEQSKEVAIRIFQGCQFRSVEAVQEITEYAKSIPGFVNLDLNDQVTLLKYGVHEIIYT
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Rattus norvegicus clone CH230-222E15, *** SEQUENCING IN PROGRESS
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                                                                                                                                                                                                                                               Z (Dases 1 to 2063)
Zhou,J., Wilson,K.M. and Medh,J.D.
Direct Submission
Submitted (27-JUL-2011) Internal Medicine, The University of Iowa,
200 Hawkins Drive, Iowa, IA 52242, USA
Location/Qualifiers
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Cercopithecidae,
                                                                       1 (bases 1 to 2063)
Zhou, J., Wilson, K.M. and Medh, J.D.
Genetic analysis of four novel peroxisome proliferator activated
Teceptor-gamma splice variants in monkey macrophages
Biochem. Biophys. Res. Commun. 293 (1), 274-283 (2002)
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Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae,
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                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Macaca fascicularis"
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1. .2063
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                                                    Cercopithecinae; Macaca.
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                                                                                         ΔυΖΒ DP MRNA linear PRI 24-JUN-2002 gamma 4 (PPARgamma4) mRNA, complete cds.
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ALAMILYDOSIKSFPLITAKARARLILTGKTTDKSPSFVIYDVMSLWMCBDEKKFKITTPL
OBOSKEVAR I FIGOGORFSVEAVQE TEXAKS I FORVILDLANDQYTLLKYGVHBITYPL
MLASLANKDGVFISBGQGFWTREFLKSLRKPFQDFMSPKFERAVKFNALELDDSDLAI
PIAVIILSCDRPGLLNVKPIEDIQDNLLQALELQLKINHPESSQLFAKLLQKMTDLRQ
I VFBVVQLLQVIKKTETDMSLHPLLQBIYKDLY"
1 452 C 438 g 515 t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /db_xref="G1:21552435"
/translation="MKGFSEITMVDTEMPFWPTNFGISSVDLSVMDDHSHSFDIKPFT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TVDFSSISAPHYEDI PFTRTDPMVADYKYDLKLQEYQSAIKVBPASPPYYSEKTÖLYN
KPHEEPSNSLMAIECRVCGDKASGFHYGVHACEGCKGFFRRTIRLKLIYDRCDLNCRI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 (bases 1 to 2028)
Zhou,J., Wilson,K.M. and Medh,J,D.
Direct Submission
Submitted (27-JUL-2001) Internal Medicine, The University of Iowa,
                                                                                                                                                                                                                                                                                              Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae; Cercopithecinae; Macaca.

1 (Dases 1 to 2028)
Zhou J., Wilson, K.M. and Medh, J.D.
Genetic analysis of four novel peroxisome proliferator activated receptor-gamma splice variants in monkey macrophages
Biochem. Biophys. Res. Commun. 293 (1), 274-283 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Macaca fascicularis peroxisome proliferator-activated receptor gamma 6 (PPARgamma6) mRNA, complete cds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Macaca fascicularis"
/db xref="taxon:9541"
/cell_type="macrophage"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          200 Hawkins Drive, Iowa, IA 52242, USA
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               note="transcription factor"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      type="macrophage"
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gene="PPARgamma4"
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Macaca fascicularis
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Davila, M.L., Davis, C., Davy-Carroll, L., Dederich, D.B.,
Delaney, K.R., Delgado, O., Denn, A.L., Ding, Y., Dinh, H.H.,
Douthwaite, K.J., Drager, H., Dugan-Rochas, S., Dubrin, K.J.,
Earnhart, C., Eddar, D., Edwards, C.C., Elhaj, C., Escotto, M.,
Earnhart, C., Eddar, D., Edwards, C.C., Elhaj, C., Escotto, M.,
Falls, T., Ferraguto, D., Flagg, N., Ford, J., Foster, P., Frantz, P.,
Gorrell, J.H., Guevara, W., Garner, T., Garza, N., Gill, R.,
Harris, C., Harris, K., Hart, M., Havlak, P., Hawes, A., Hernandez, J.,
Hernandez, O., Hodgson, A., Hogues, M., Holloway, C., Hollins, B.,
Jacobson, B., Jia, Y., Johnson, R., Jolivet, S., Joudah, S.,
Karlsson, E., Kelly, S., Khan, U., King, L., Korvah, J.,
Kovar, C.,
Katovic, J., Kureshi, A., Landry, N., Leal, B., Lewis, L.C.
Li, J., Li, Z., Lichtarge, O., Lieu, C., Liu, J., Liu, W., Loulseged, H.,
Massey, E., Mawhiney, E., McLeod, M.P., Meador, M., Mei, G.,
Massey, E., Mawhiney, E., McLeod, M.P., Meador, M., Myen, A.,
Nguyen, N., Nickerson, E., Nowlean, P., Neutson, N., Nguyen, N.,
Nguyen, N., Nickerson, E., Neutson, N., Nguyen, A., Nguyen, N.,
Nguyen, N., Nickerson, E., Neutson, N., Nguyen, A., Sherer, Y.,
Rives, M., Rojaba, R., Primus, E., Pu, L.L., Quiles, M.,
Scherer, S., Scott, G., Shen, H., Shoosherari, N., Thomas, S.,
Usmani, K., Vasquez, L., Versen, Y., Tenerisa, K., Tang, H.,
Tansey, J., Taylor, C., Taylor, P., Tamerisa, A., Tamerisa, K., Tang, H.,
Millams, G., Williamson, A., Warten, R., Washington, C., Wu, Y., Wu, W
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NOTE: This is a 'working draft' sequence. It currently consists of 52 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (13.JUL-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
On Jul 11, 2002 this sequence version replaced gi:17974449.
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Sequencing vector: plasmid;
Assembly program: Phrap; version 0.990329
Consensus quality: 82376 bases at least Q40
Consensus quality: 88376 bases at least Q40
Consensus quality: 88830 bases at least Q30
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Center code: BCM
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COMMENT

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25645: contig of 1413 bp in length 2574s: gap of unknown length 27575: contig of 1830 bp in length 27675: gap of unknown length 27677: gap of unknown length 29667: contin of """
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: gap of unknown length

: contig of 2875 bp in 1...
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bp in length
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contig of 1451 bp in length gap of unknown length contin ...
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30373: contig of 1206 bp in length
30473: gap of unknown length
33015: contig of 2542 bp in length
33115: gap of unknown length
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bp in length
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contig of 1551 bp in length
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bp in length
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unknown length
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gap of unknown length
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gap of unknown length
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contig of 1098 bp in length
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of 2886 h
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                                                                                                                                                                             unknown
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contig of 1053
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contig of 2267
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contig of 1883
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NOTE: This is a 'working draft' sequence. It currently consists of 55 contigs. The true order of the pieces is not known and thehar order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (22-FEB-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

3 (bases 1 to 182241)
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Sequencing vector: plasmid;
Assembly program: Phrap; version 0.990329
Consensus quality: 123458 bases at least Q40
Consensus quality: 116923 bases at least Q30
Consensus quality: 140922 bases at least Q30
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1521: gap of unknown length
2743: contig of 1222 bp in length
3843: gap of unknown length
3897: contig of 1054 bp in length
3997: gap of unknown length
5369: contig of 1372 bp in length
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Center code: BCM
Web Site: http://www.hgsc.bcm.tmc.edu/
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Center project name: GRPN
Center clone name: CH230-45P12
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Direct Submission
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Rattus norvegicus clone CH230-45P12, *** SEQUENCING IN PROGRESS
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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Homo sapiens chromosome X clone bWXD173, *** SEQUENCING IN PROGRESS
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On Jun 13, 2002 this sequence version replaced gi:2944106.
Current status of this project is available at:
'http://www.ibc.wustl.edu/cgm/seq_projects.html'
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Applied Biosystems Division of Perlin Elmer Corp.,
850 Lincoln Center Drive,
Carer City, CA 94404 USA
e-mail: ellson@genseq.apldbio.com
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gap of unknown length
contig of 10022 bp in length
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Pred. No. 52;
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hunqueryGesanger.ac.uk Clone requests: clonerequestGesanger.ac.uk
On May 3, 2002 this sequence version replaced gi:20386306.

During sequence assembly data is compared from overlapping clones.

Where differences are found these are annotated as variations
together with a note of the overlapping clone name. Note that the
variation annotation may not be found in the sequence submission
corresponding to the overlapping clone, as we submit sequences with
only a small overlapping clone, as we submit sequences with
only a small overlapping clone, as we submit sequences with
This sequence was finished as follows unless otherwise noted: all
regions were either double-stranded or sequenced with an alternate
chemistry or covered by high quality data (i.e., phred quality >=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ..
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                        St. Louis, W0 6108 USA
e-mail: states@ibc.wustl.edu.
* NOTE: This is a 'working draft' sequence. It currently
* Consists of 2 contigs. Gaps between the contigs
* are represented as runs of N. The order of the pieces
* is believed to be correct as given, however the sizes
* of the gaps between them are based on estimates that have
* provided by the submittor.
* This sequence will be replaced
* by the finished sequence as soon as it is available and
* the accession number will be preserved.

* I 195298: contig of 195298 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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                                                  Washington University School of Medicine, Box 8232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          195299 195398: gap of 100 bp 195399 206156: contig of 10758 bp in length.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100 others
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Pred. No. 62;
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                                                                                                                                                                                                                                     David J. States,
Institute for Biomedical Computing
Washington University in St. Louis
700 South Euclid Ave.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="X"
                                                                                                                               e-mail: buddy@qenetics.wustl.edu
                         Center for Genetics in Medicine,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
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                                                                         4566 Scott Avenue,
St. Louis, MO 63110, USA
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AL672032.6 GI:20428914
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Best Local Similarity 76.3%;
Matches 29; Conservative
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TITLE
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30); an attempt was made to resolve all sequencing problems, such one plasmid subclone or more than one Mi3 subclone; and the assembly was confirmed by restriction one Mi3 subclone; and the absembly was confirmed by restriction digest. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em., EMBL; Sw.; SWISSPROT; Tr.; TREMBL, Wp.; WORNPEP; Information on the WORNPEP http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome X, constructed by the Sanger Centre Chromosome X Mapping
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0
                                                                                                                                                                                                                                                                                                                                                                Group. Purther information can be found at http://www.sanger.ac.uk/HGP/Chrx RP11-308B5 is from the library RPCI-11.2 constructed by the group of Pieter and Jong. For further details see http://www.chori.org/bacpac/home.htm
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62375 a 44037 c 43724 g 59181 t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /chromosome="X"
/clone="RP11-308B5"
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Matches 29; Conservative
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Human PPARgamma co Peroxisome prolife Murine alpha-1,3-f Human PPAR gamma P Human PPAR gamma g Human PPAR gamma g Human pPAR gamma g Human colon tumour Human colon tumour Human colon tumour

Title: Perfect score:

Run on:

Scoring table: Sequence:

Searched:

ΩC

Database

Human PAX8e9(-exon Human PAX8e9-PPARg Human PPAR-gamma P

Human PAX8e7-PPARG

PAX8e9-PPARgammae1

Human peroxisome p Human PPARgamma cD

Peroxisome prolife
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Human reproductive
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CDNA encoding nove
Human DNA sequence
Human PARRgamma-PA
Human PAX8 CDNA se
Human PAX8 CDNA se

Bovine PPAR coding Rat PPAR-gamma A/B Mouse PPAR-gamma A

Human cDNA sequenc

Human peroxisome p Peroxisome prolife

Mouse peroxisome Senomic sequence

Murine cDNA isolat

Mouse secreted

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PAX8-PPARgammal; oncogene; cytostatic; PAX8; PPARgammal; cancer; follicular carcinoma; PAX8e8-PPARgammael; human; ss.
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AAZ92645
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14-AUG-2000; 2000US-0225079
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                                                                                                                                                                                                                                                                                                                                                                                                                                               / SIDS2/gogdata/geneseq/geneseqn-emb1/Nk1993.DAT:
/ SIDS2/gogdata/geneseq/geneseqn-emb1/Nk1994.DAT:
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Copyright (c) 1993 - 2003 Compugen Ltd.
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24-JUL-1998;
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                                                                                                                                                                                                                                                                      AAX19066;
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                                                                                                                                                                                                                        RESULT 3
                                                                                                                                                                                                                                    AAX19066
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                                                                                      The invention relates to an oncogene designated PAX8-PPARgammal that concains a PAX8 coding region fused to PPARgammal coding region. The PAX8-PPARgammal polypeptides can be expressed by standard recombinant methodology. A PPARgamma ligand or agent is useful for treating a subject having a disorder characterized by the presence of a PAX8-PPARgammal, where the disorder is cancer, e.g. follicular carcinoma. The PAX8-PPARgammal molecules are also useful for providing nucleotide and amino acid sequences useful for detecting the above disease. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      contains a PAX8 coding region fused to PPARgammal coding region. The PAX8-PPARgammal polypeptides can be expressed by standard recombinant
                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention relates to an oncogene designated PAX8-PPARgammal that
                                 useful for detecting and
                                                                                                                                                                                    present sequence represents the nucleotide sequence including and surrounding the fusion juncture in the PAX8e8-PPARgammael DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PAX8-PPARgammal; oncogene; cytostatic; PAX8; PPARgammal; cancer;
                                                                                                                                                                                                                                                                     ·,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                oncogene and oncoprotein, useful for detecting
n tumors or cancers, e.g. follicular carcinoma
                                              treating certain tumors or cancers, e.g. follicular carcinoma
                                                                                                                                                                                                                                             Length 42;
                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 follicular carcinoma; PAX8e8-PPARgammae1; human; ss.
                                                                                                                                                                                                                                                                                                         1 CGGGCCAGGCCCTCTCTCAGAAATGACCATGGTTGACACA 42
                                                                                                                                                                                                                                                                                           1 CGGCCCAGGCCCTCCTCAGAAATGACCATGGTTGACACAG 42
                                                                                                                                                                                                                                             100.0%; Score 42; DB 22;
                                                                                                                                                                                                                                                         Pred. No. 3.2e-08
                                                                                                                                                                                                                     Sequence 42 BP; 10 A; 14 C; 11 G; 7 T; 0 other;
                                                                                                                                                                                                                                                        1 Similarity 100.0%; Pred. No. 3.2 42; Conservative 0; Mismatches
                                  New PAX8-PPARc1 oncogene and oncoprotein,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           reating certain tumors or cancers, e.g.
                                                                                                                                                                                                                                                                                                                                                                                                                                               Human PAX8e8-PPARgammael cDNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (BGHM ) BRIGHAM & WOMENS HOSPITAL INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 1; Page 106-109; 145pp; English.
                                                                    Claim 21; Page 118; 145pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                         AAH76282 standard; cDNA; 2523 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        18-JAN-2001; 2001WO-US01664.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2C JAN-2000; 2000US-0177109.
14-AUG-2000; 2000US-0225079.
                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2523
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Kroll TG, Fletcher JA;
WPI; 2001-514487/56.
P-PSDB; AAB85797.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2001-514487/56.
                                                                                                                                                                                                                                           Ouery Match
Best Local Similarity
Matches 42; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New PAX8-PPARcl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO200152789-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    virus (HIV) treatment, insulin resistance, non-insulin-dependent diabetes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            mellitus (NIDDM), polycystic ovary syndrome, diseases of the gastrointestinal (GI) tract, inflammatory bowel disease, Crohn's disease,
methodology. A PPARgamma ligand or agent is useful for treating a subject having a disorder characterized by the presence of a PAXB-PPARgamma1, where the disorder is cancer, e.g. follicular carcinoma. The PAXB-PPARgamma1 molecules are also useful for providing nucleotide and amino acid sequence useful for detecting the above disease. The present sequence represents a human PAXBeB-PPARgammae1 polypeptide encoding cDNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human; peroxisome proliferator activated receptor gamma; PPAR-gamma; regularory sequence; promoter; obesity; anorexia; lipoma; cachexia; lipodystrophy; liposarcoma; human immunodeficiency virus; HIV; insulin resistance; non-insulin-dependent diabetes mellitus; polycystic ovary syndrome; gastrointestinal tract; Crohn's disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Newly isolated nucleic acid comprising a control region of a human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          peroxisome proliferator activated receptor (PPAR) gamma gene useful for identifying modulators that are useful in treating diseases associated with abnormal levels of human PPAR-gamma gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present invention describes an isolated, purified or enriched
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            inflammatory bowel disease; ulcerative colitis; bowel cancer; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Score 42; DB 22; Length 2523; 100.0%; Pred. No. 8.2e-08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                 Sequence 2523 BP; 643 A; 723 C; 614 G; 543 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1067 CGGGCCAGGCCCTCTCTCAGAATGACCATGGTTGACACAG 1108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CGGGCCAGGCCCTCTCAGAAATGACCATGGTTGACACAG 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human PPAR-gamma intron B, exon 1 and intron 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Saladin RS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ВР.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAX19066 standard; DNA; 695
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     98WO-US15411
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Auwerx J, Briggs MR,
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Matches 42; Conserv
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9 GCCCTCCTCTCAGAAATGACCATGGTTGACACAG

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ulcerative colitis and bowel cancer. The nucleic acids are useful for studying the role of the PPAR-gamma gene in various diseases and disorders. The structure of PPAR-gamma enables genetic studies of PPAR-gamma mutations in humans, and evaluation of its role in disorders like insulin resistance, NIDDM, and diseases associated with altered adipose tissue function, like obesity and lipodystrophic syndromes. The nucleic acids are also useful for gene therapy and the production of transgenic animals, which are useful in screening assays. The control regions of the nucleic acids enable screening for modulators of the human PPAR-gamma gene, which are useful in designing drugs for treating disorders or diseases associated with the level of PPAR-gamma gene expression.

The present sequence represents the human PPAR-gamma intron B, exon 1 and intron 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              energy
                                                                                                                                                                                                                                                                                                              Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This sequence encodes the human peroxisome proliferator activated receptor-gammal (PPAR-gammal),
                                                                                                                                                                                                                                                                                                          0;
                                                                                                                                                                                                                                                                         DB 20; Length 695;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nuclear receptor agonist; antagonist; identification; PPAR; peroxisome proliferator activated receptor; ss.
                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                       Sequence 695 BP; 196 A; 148 C; 130 G; 221 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 1811 BP; 510 A; 433 C; 422 G; 446 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Identifying nuclear receptor agonists and antagonists
                                                                                                                                                                                                                                                                       Score 28.4; DB 2
Pred. No. 0.035;
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                                                                                                                                                                                                                                                                                                        0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                      424 TCCTTTCAGAATGACCATGGTTGACAG 453
                                                                                                                                                                                                                                                                                                                                          13 TCCTCTCAGAATGACCATGGTTGACACAG 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Moller DE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human PPAR-gammal coding sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure; Fig 9b; 60pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAX36522 standard; cDNA; 1811 BP
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                                                                                                                                                                                                                                                                         67.6%;
ilarity 96.7%;
Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 'MERI ) MERCK & CO INC.
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P-PSDB; AAY05471.
                                                                                                                                                                                                                                                                                       Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAX36522;
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PPARgammal, where the disorder is cancer, e.g. follicular carcinoma. The PAKR-PPRAgammal molecules are also useful for providing nucleotide and amino acid sequences useful for detecting the above disease. The present sequence represents a human PPARgamma polypeptide encoding cDNA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New PAX8-PPARc1 oncogene and oncoprotein, useful for detecting and treating certain tumors or cancers, e.g. follicular carcinoma
                                                                                                                                                                                                                              PAX8-PPARgammal; oncogene; cytostatic; PAX8; PPARgammal; cancer;
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85.3%; Pred. No. 0.45;
ive 0; Mismatches 5; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 1811 BP; 510 A; 433 C; 422 G; 446 T; 0 other;
158 GCCGTGGCCGCAGAAATGACCATGGTTGACACAG 191
                                                                                                                                                                                                                                                 follicular carcinoma; PPARgamma; human; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         158 GCCGTGGCCGCAGAATGACCATGGTTGACACAG 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9 GCCCTCCTCTCAGAAATGACCATGGTTGACACAG 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; Page 137-139; 145pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (BGHM ) BRIGHAM & WOMENS HOSPITAL INC.
                                                                                                                                                                                                                                                                                                                Location/Qualifiers
173..1609
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ABN95714 standard; DNA; 1811 BP
                                                                                              AAH76296 standard; cDNA; 1811
                                                                                                                                                                                             Human PPARgamma cDNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          20-JAN-2000; 2000US-0177109
14-AUG-2000; 2000US-0225079
                                                                                                                                                             29-OCT-2001 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Kroll TG, Fletcher JA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2001-514487/56.
P-PSDB; AAB85802.
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Matches 29; Conserv
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                                                                                                                                                                                                                                                                                 Homo sapiens.
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                                                                                                                              AAH76296;
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                                                                                AAH76296
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ch 61.9%; Score 26; DB 20; Length 1811; 1 Similarity 85.3%; Pred. No. 0.45; 29; Conservative 0; Mismatches 5; Indels (

Query Match Best Local Similarity

Matches

Homo sapiens

11-APR-2002

Horne D,

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Mammal; human, rhesus monkey; baker's yeast; fission yeast; Norway rat; mouse; Chinese hamster; African clawed frog; fruit fly, dog; leukaemia; cancer; lymphoma; neuroblastoma; autoimmune disorder; cell proliferation; nervous system disorder; inflammatory disorder; cell differentiation; ds; angiogenesis; stem cell growth factor; activin; inhibin; cartilage; burn; genetic disorder; bone regeneration; tendon; ligament; tissue repair; cytostatic; antirheumatic; antiarthritic; vulnerary; antiinflammatory;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           antibacterial, immunosuppressive, vasotropic, antiparkinsonian, neuroprotective, osteopathic, antidiabetic, antiasthmatic, antiallergic,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present sequence encodes a human peroxisome proliferator-activated receptor gamma (PPAR-gamma) polypeptide. PPAR are orphan receptors, and may play a role in proliferative and differentiation aspects of cancer. The PPAR-gamma polynucleonid is useful for detecting a mRNA transcript that encodes PPAR polypeptide. It is also useful for detecting hybrid formation. The PPAR-gamma polypeptide is useful for detecting hybrid formation. The PPAR-gamma polypeptide is useful for detecting hybrid formation.
                                              "peroxisome proliferator-activated receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Novel isolated and purified polynucleotide encoding human peroxisome proliferator-activated receptor gamma polypeptide useful in diagnostics, drug design and therapeutics -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 22; Length 1844;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Seguence 1844 BP; 543 A; 433 C; 421 G; 447 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human full-length polynucleotide sequence #78.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0.46;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           158 GCCGTGGCCGCAGAATGACCATGGTTCACACAG 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9 GCCCTCCTCTCAGAATGACCATGGTTGACACAG 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            immunostimulant; analgesic; gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 26;
Pred. No. (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 3; Column 43-48; 29pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAS44653 standard; DNA; 2295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61.9%;
                                                                                                                                                                                                            93US-0134557
                                                                                                                                                                                                                                                           93US-0134557,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            85.3%;
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/product= "
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  179..1609
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 61.9
Best Local Similarity 85.3
Matches 29; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        design and therapeutics.
                                                                                                                                                                                                                                                                                                                                                       Blumberg B;
                                                                                                                                                                                                                                                                                                        DEV CORP.
                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2001-234517/24.
                                                                                                                                                                                                                                                                                                                                                                                                                            P-PSDB; AAB67656.
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                                                                                                                                                                                                            08-OCT-1993;
                                                                                                                                                                                                                                                         08-OCT-1993;
                                                                                                                                                                                                                                                                                                        (ARCH-) ARCH
                                                                                                                 US6200802-B1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens
                                                                                                                                                                13-MAR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            18-DEC-2001
                                                                                                                                                                                                                                                                                                                                                       Greene ME,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    07-SEP-2001
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AAS44653/c
ID AAS446
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CDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            progression of liver cancer, hepatocellular carcinoma or metastatic liver tumour in a patient, and differentiating metastatic liver cancer from hepatocellular carcinoma in a patient, involving detecting the level of expression of two or more genes represented in ABN93503-ABN97455 in a cytostatic activity. The method is invention has hepatoropic, and cytostatic activity. The method is useful for diagnosing and detecting the progression of liver cancer, hepatocellular carcinoma and metastatic liver carcinoma in a patient. The method is useful for identifying expression profiles which serve as useful diagnostic markers as well as markers that can be used to monitor disease states, disease progression,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention relates to a novel method for diagnosing and detecting the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    drug toxicity, drug efficacy and drug metabolism.
Note: The sequence data for this parent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pot_sequences.
                                                                                   metastatic liver tumour, cytostatic, expression profile, disease state, disease progression, drug toxicity, drug efficacy, drug metabolism.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               proliferator-activated receptor gamma; PPAR-gamma; cancer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Diagnosing and detecting the progression of liver cancer, hepatocellular carcinoma or metastatic liver tumor in a patient, involves detecting the level of expression of two or more genes in
                                                             Gene; liver cancer; ds; hepatocellular carcinoma; hepatotropic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 24; Length 1811;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human peroxisome proliferator-activated receptor gamma DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Seguence 1811 BP; 510 A; 433 C; 422 G; 446 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                             Vockley JG;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ις
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 26; DB 2
Pred. No. 0.45;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               158 GCCGTGGCCGCAGAATGACCATGGTTGACACAG 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9 GCCCTCCTCTCAGAATGACCATGGTTGACACAG 42
                   Gene #2212 used to diagnose liver cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                             Peres-Da-Silva S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ID NO 2212; 298pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAF55663 standard; DNA; 1844
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ouery Match
Best Local Similarity 85.3%;
Matches 29; Conservative
                                                                                                                                                                                                                                                                                                     02-OCT-2001; 2001WO-US30589
                                                                                                                                                                                                                                                                                                                                                  02-OCT-2000; 2000US-237054P
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                                                                                                                                                                                                                                                                                                                                                                                                 (GENE-) GENE LOGIC INC
                                                                                                                                                                                                                                                                                                                                                                                                                                             Alvares C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             tissue sample
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2002-426119/45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human; peroxisome
                                                                                                                                                                                                          WO200229103-A2
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Homo sapiens

Key

29-MAY-2001

AAF55663;

RESULT 7 AAF55663

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Claim 1; SEQ

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Gaps

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Indels

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18-MAY-2000; 7-JUN-2000;

Drmanac R;

detection

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The invention relates to an oncogene designated PAX8-PPARgammal that contains a PAX8 coding region fused to PPARgammal coding region. The PAX8-PPARgammal polypeptides can be expressed by standard recombinant methodology. A PPARgammal igand or agent is useful for treating a subject having a disorder characterized by the presence of a PAX8-PPARgammal, where the disorder is cancer. e.g. follicular carcinoma. The PAX8-PPARgammal molecules are also useful for providing nucleotide and amino acid sequences useful for detecting the above disease. The present sequence represents the nucleotide sequence including and surrounding the translocation fusion juncture in the PAX867-PPARgammael
                                                                                                                                                                                                                                                                                                                                                                                                                                              New PAX8-PPARc1 oncogene and oncoprotein, useful for detecting and treating certain tumors or cancers, e.g. follicular carcinoma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      oncogene; cytostatic; PAX8; PPARgammal; cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            follicular carcinoma; PAX8e7-PPARgammae1; human; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 25.2; DB 22;
Pred. No. 0.41;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 42 BP; 12 A; 11 C; 12 G; 7 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5 cracccccregregradaaneaccarecricacacaca 42
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human PAX8e7-PPARgammae1 cDNA sequence.
                                                                                                                                                                                                                                                                              (BGHM ) BRIGHAM & WOMENS HOSPITAL INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Cocation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 21; Page 118; 145pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAH76281 standard; cDNA; 2334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     60.08;
78.98;
                                                                                                                                                             18-JAN-2001; 2001WO-US01664.
                                                                                                                                                                                                         20-JAN-2000; 2000US-0177109.
14-AUG-2000; 2000US-0225079.
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3..41
/*tag=
                                                                                                                                                                                                                                                                                                                           Fletcher JA;
                                                                                                                                                                                                                                                                                                                                                                         WPI; 2001-514487/56.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PAX8-PPARgamma1;
                                                                  WO200152789-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WO200152789-A2
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                                                                                                              26-JUL-2001
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                                                                                                                                                                                                                                                                                                                        Kroll TG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAH76281;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       QQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    as multiple sclerosis, connective tissue disease, rheumatoid arthritis, diabetes multiple sclerosis, connective tissue disease, rheumatoid arthritis, diabetes multius, allergic rhinitis, asthma and eczema, nervous system disorders such as Parkinson's disease, Alzheimer, disease, huntingron's chorea, amyotrophic lateral sclerosis, spinal muscular atrophy and Wernicke disease, inflammatory disorders such as nephritis, Crohn's disease, ischemaia-repertusion injury, shock, sepsis and inflammatory bowel disease. The sequences exhibit activity relating to angiogenesis, cell proliferation, cell differentiation, stem cell growth factor, activin or inhibin. Therefore they can be used to manipulate stem cells in culture to give rise to neuroepithelial cells that can be used to augment or replace cells damaged by illness, accidental damage or genetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       disorders. The sequences may also be used for regeneration of bone, cartilage, tendons and ligaments and in tissue repair and burn healing. Note: Some sequences for this patent did not form part of the printed specification, but were obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequences AAS44576-AAS44919 represent full-length polynucleotides and contig polynucleotides encoding polypeptides of the invention. The DNA and protein sequences are useful for the treatment, diagnosis and prevention of various types of disorder in a mammalian subject such as a human, dog, monkey, mouse, hamster or rat. The disorders include cancers such as leukaemia, lymphoma and neuroblastoma, autoimmune disorders such
                                                                                                                                                                                      Ren F;
° Xu C;
                                                                                                                                                                                                                                                                                                                                                                  Novel polypeptides and nucleic acids obtained from cDNA libraries prepared from various human tissues, for diagnosis, treatment of cancer, neurological, inflammatory disorders and for use in arrays for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PAX8-PPARgammal; oncogene; cytostatic; PAX8; PPARgammal; cancer; follicular carcinoma; PAX867-PPARgammael; human; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PAX8e7-PPARgammael translocation fusion juncture 1 DNA sequence.
                                                                                                                                                                                                       Zhang J, Zhao QA, Ren F
Ma Y, Wang D, Chen R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ·;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 2295 BP; 525 A; 606 C; 565 G; 599 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1654 GCCGTGGCCGCAGAATGACCATGGTTGACACAG 1621
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Mismatches
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                                                                                                                                                                                                    Tang YT, Liu C, Zhou P, Asundi V,
Xue AJ, Yang Y, Wehrman T, Wang J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           claim 1; SEQ ID No 78; 153pp; English.
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              2000US-0515126.
2000US-0577409.
2000US-0597707.
2000US-0616807.
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es 29; Conserv
                                                                                                                                                        (HYSE-) HYSEQ INC
                                                                                                                                                                                                                                                                                                                        P-PSDB; AAU27753
                   28-FEB-2000;
                                                                                   14-JUL-2000;
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Homo sapiens

Key

29-OCT-2001

AAH76284;

'y Match Matches

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Length 42; Indels

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P-PSDB; AAB85801.
                                                                                                                                                                       Local Similarity
tes 28; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO200152789-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      14-AUG-2000;
                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens.
                                                                                                                                         Sequence 42
                                                                                                                                                                                                                                                                                                                29-0CT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     26-JUL-2001
                                                                                                                                                                                                                                                                                             AAH76294;
                                                                                                                                                              Query Match
                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                    RESULT 12
AAH76294
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                                                                                                                                                                                                                                                                                                                                                                                                          Key
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                                                                                                                                      The invention relates to an oncogene designated PAX8-PPARgammal that contains a PAX8 coding region fused to PPARgammal coding region. The PAX8-PPARgammal coding region. The PAX8-PPARgammal properties can be expressed by standard recombinant methodology. A PPARgamma ligand or agent is useful for treating a subject having a disorder characterized by the presence of a PAX8-PPARgammal, where the disorder is cancer, e.g. follicular carcinoma. The PAX8-PPARgammal molecules are also useful for providing nucleotide and amino acid sequences useful for detecting the above disease. The present sequence represents a human PAX887-PPARgammael polypeptide
                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New PAX8-PPARcl oncogene and oncoprotein, useful for detecting and treating certain tumors or cancers, e.g. follicular carcinoma
                                                                                       New PAX8-PPARc1 oncogene and oncoprotein, useful for detecting and treating certain tumors or cancers, e.g. follicular carcinoma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PAX8-PPARgammal; oncogene; cytostatic; PAX8; PPARgammal; cancer; follicular carcinoma; PAX8e9-PPARgammael; human; ss.
                                                                                                                                                                                                                                                                                             0
                                                                                                                                                                                                                                                                         DB 22; Length 2334;
                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                      Sequence 2334 BP; 614 A; 650 C; 573 G; 497 T; 0 other;
                                                                                                                                                                                                                                                                                            œ
                                                                                                                                                                                                                                                                                                                                                                                                                                                 PAX8e9-PPARgammael fusion juncture DNA sequence.
                                                                                                                                                                                                                                                                                                                            882 CTACCCCGTGGTGGCAGAAATGACCATGGTTGACACAG 919
                                                                                                                                                                                                                                                                                                               5 CCAGGCCCTCCTCAGAAATGACCATGGTTGACACAG 42
                                                                                                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                                        Score 25.2;
Pred. No. 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (BGHM ) BRIGHAM & WOMENS HOSPITAL INC.
                  (BGHM ) BRIGHAM & WOMENS HOSPITAL INC.
                                                                                                                     Claim 1; Page 100-104; 145pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
                                                                                                                                                                                                                                                                                             ô
                                                                                                                                                                                                                                                                                                                                                                                      BP.
                                                                                                                                                                                                                                                                        60.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        20-JAN-2000; 2000US-0177109.
14-AUG-2000; 2000US-0225079.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2001WO-US01664
14-AUG-2000; 2000US-0225079
                                                                                                                                                                                                                                                                                                                                                                                      AAH76286 standard; DNA; 42
                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                             30; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /*tag=
                                       Fletcher JA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Fletcher JA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2001-514487/56.
                                                         WPI; 2001-514487/56.
                                                                                                                                                                                                                                                                                  Similarity
                                                                    P-PSDB; AAB85793
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          P-PSDB; AAB85798
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WO200152789-A2
                                                                                                                                                                                                                                   encoding cDNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      18-JAN-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                               29-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  26-JUL-2001
                                       TG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Kroll TG,
                                                                                                                                                                                                                                                                                                                                                                                                          AAH76286:
                                                                                                                                                                                                                                                                         Query Match
Best Local S
                                                                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                                                                                                   RESULT 11
                                                                                                                                                                                                                                                                                                                                                                              AAH76286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Key
8
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The invention relates to an oncogene designated PAX8-PPARgammal that contains a PAX8 coding region fused to PPARgammal coding region. The PAX8-PPARgammal polypeptides can be expressed by standard recombinant methodology. A PPARgamma ligand or agent is useful for treating a subject having a disorder characterized by the presence of a PAX8-PARgammal, where the disorder is cancer, e.g. follioular carcinoma. The PAX8-PPARgammal molecules are also useful for providing nucleotide and amino acid sequences useful for detecting the above disease. The
                                                                                                                                                                                                            subject having a disorder characterized by the presence of a PAX8-PPARgammal, where the disorder is cancer, e.g. follicular carcinoma. The PAX8-PPARgammal molecules are also useful for providing nucleotide and amino acid sequences useful for detecting the above disease. The present sequence represents the nucleotide sequence including and surrounding the fusion juncture in the PAX8e9-PPARgammael DNA.
                                                                    The invention relates to an oncogene designated PAX8-PPARgammal that contains a PAX8 coding region fused to PPARgammal coding region. The PAX8-PPARgammal polypeptides can be expressed by standard recombinant methodology. A PPARgamma ligand or agent is useful for treating a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        useful for detecting and follicular carcinoma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PAX8-PPARgammal; oncogene; cytostatic; PAX8; PPARgammal; cancer; follicular carcinoma; PAX8e9(-exon 8)-PPARgammae1; human; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BP; 12 A; 10 C; 13 G; 7 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human PAX8e9(-exon 8)-PARgammae1 cDNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            6.6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GCCCTCCTCTCAGAATGACCATGGTTGACACAG 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9 decartegrecadadadreaccartegracacae 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New PAX8-PPARc1 oncogene and oncoprotein,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 24.4;
Pred. No. 0.9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  treating certain tumors or cancers, e.g.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (BGHM ) BRIGHAM & WOMENS HOSPITAL INC.
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161..2596
Claim 21; Page 119; 145pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                82.4%;
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(first entry)

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Human, Fas, PCR primer, reporter gene, cancer, autoimmune disease, mouse fibroblast L929; human cancer cell HeLa; receptor; PPAR alpha; PPAR gamma, PPAR delta; ss.
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  1177 GGCATGGTGGCAGAAATGACCATGGTTGACACAG 1210
                                                                                                                                                                                                                                                               Human PPAR-gamma PCR sense primer F3.
                                                                                                                        AAX00271 standard; DNA; 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (ONOY ) ONO PHARM CO LID.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hagiya H, Minami M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 1999-095737/08
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                                                                                                                                                                                                                   25-MAR-1999
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                                                                                                                                                                                                                                                                                                                                                                                                           Synthetic
                                                                                                                                                                    AAX00271;
                                                                         RESULT 14
                                                                                               AAX0027
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                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New PAX8-PPARc1 oncogene and oncoprotein, useful for detecting and treating certain tumors or cancers, e.g. follicular carcinoma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PAX8-PPARgammal; oncogene; cytostatic; PAX8; PPARgammal; cancer; follicular carcinoma; PAX8e9-PPARgammael; human; ss.
represents a human PAX8e9(-exon 8)-PPARgammael
                                                                                                                                                                  0;
                                                                                                                   DB 22; Length 2596;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 24.4; DB 22; Length 2625;
Pred. No. 2.4;
0; Mismatches 6; Indels 0;
                                                                                                                                                                  Indels
                                                                       Sequence 2596 BP; 660 A; 745 C; 672 G; 519 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 2625 BP; 662 A; 761 C; 646 G; 556 T; 0 other;
                                                                                                                                                                  9
                                                                                                                 Score 24.4; DB Pred. No. 2.3; 0; Mismatches
                                                                                                                                                                                                                                                          1148 GGCATGGTGGCAGAATGACCATGGTTGACACAG 1181
                                                                                                                                                                                                              GCCCTCCTCTCAGAATGACCATGGTTGACACAG 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human PAX8e9-PPARgammael cDNA sequence.
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1..2625
                                                                                                                                                                                                                                                                                                                                                                                AAH76283 standard; cDNA; 2625
                                                                                                                 Query Match
Best Local Similarity 82.4%;
Matches 28; Conservative
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l Similarity 82.4%;
28; Conservative
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14-AUG-2000; 2000US-0225079.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                        polypeptide encoding cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Kroll TG, Fletcher JA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2001-514487/56.
P-PSDB; AAB85795.
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Best Local Similarity
    present sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO200152789-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 encoding cDNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           :9-OCT-2001
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                                                                                                                                                                                                                                                                                                                               RESULT 13
AAH76283
ID AAH76283
XX AAH76283
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Tajima H;

97JP-0171440.

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amino-acid sequence with a promoter downstream from the Gal 4 protein response sequence, as well as a Fas antigen membrane linking region and function expression region. Also described are: (i) a transformant coll containing both the plasmid DNA and effector protein encoding DNA; (ii) a method by using the transformant cells for screening agonists or antagonists or the intracellular receptor; and (iii) a similar method for screening intracellular receptor; and (iii) a similar method bor screening intracellular receptor agonists or antagonists in mouse fibroblast 1929 or human cancer cell Heia, with the receptor particularly being DPAR alpha, gamma or delta. The plasmid DNA and effector protein encoding DNA are used as active ingredient in drugs to treat cancer or autoimmune diseases, as is the transformant cells can also be applied in the detection of ligand of an intransclear receptor in a screening method for the intracellular receptor agonists
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                       The present invention describes plasmid DNA containing a DNA encoding an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           or antagonists, particularly in mouse fibroblast 1929 or human cancer cell HeLa with receptor being PPAR alpha, gamma or delta. The present sequence represents a PCR primer used in an example from the present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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Pred. No. 3.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               54.8%; Scot.
100.0%; Pred. No. ...
Example 2; Page 18; 43pp; Japanese
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       23
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Matches 23; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               invention.
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RESULT 15 AAD21022 ID AAD21022 standard; cDNA; 1518 BP.

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Gaps

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9 GCCCTCCTCAGAATGACCATGGTTGACACAG 42

Matches

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peroxisome proliferator activated receptors (PPAR) gammal and gamma2. The invention is useful for treating cancer and other disorders including excessive cell proliferation and viral infection. The invention is also directed to the use of PPAR gammal and gamma2 to identify compounds that are antiproliferative, antiviral and antitumour agents. The invention also relates to a method of treating cancer using a pharmaceutical composition comprising thiazolidinedione in an amount sufficient to modulate PPAR gammal and gamma2 activity. The present cDNA sequence encodes human peroxisome proliferator activated receptor (PPAR) gamma2 protein related to the invention.
                                                                                                            Human, peroxisome proliferator activated receptor gamma2, cytotoxic, antiproliferative, antiviral, cancer, cell proliferation, viral infection; pharmaceutical; thiazolidinedione; ss.
                                                                                Human peroxisome proliferator activated receptor (PPAR) gamma2 cDNA.
                                                                                                                                                                                                                                              /*tag= a
/product= "Human peroxisome proliferator activated
receptor (PPAR) gamma2 protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Use of thiazolidinedione for treating cancer and viral infections
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention relates to compounds and ligands that bind to human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ouery March 54.8%, Score 23, DB 22, Length 1518, Best Local Similarity 100.0%, Pred. No. 8.1, Matches 23, Conservative 0, Mismatches 0, Indels 0
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                                                                                                                                                                                                           Location/Qualifiers
1..1518
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Example 3; Fig 3; 17pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                     96US-016694P.
97US-0844007.
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                                                 (first entry)
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P-PSDB; AAE12868.
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18-APR-1997;
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                                               15-JAN-2002
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               AAD21022;
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0; Gaps

Search completed: January 21, 2003, 23:09:54 Job time : 129.667 secs

81 AGAAATGACCATGGTTGACACAG 103

20 AGAAATGACCATGGTTGACACAG 42

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9 GCCCTCCTCTCAGAATGACCATGGTTGACACAG 42
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                                                                     January 21, 2003, 23:03:25 ; Search time 26.3333 Seconds (without alignments) 489.130 Million cell updates/sec
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Sequence 4, F
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Sequence
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(Ggn2_6/ptodata/1/ina/5A_COMB.seq:*

(Ggn2_6/ptodata/1/ina/5B_COMB.seq:*

(Ggn2_6/ptodata/1/ina/A_COMB.seq:*

(Ggn2_6/ptodata/1/ina/6B_COMB.seq:*

(Ggn2_6/ptodata/1/ina/PcTuS_COMB.seq:*

(Ggn2_6/ptodata/1/ina/PcTuS_COMB.seq:*

(Ggn2_6/ptodata/1/ina/PcTuS_COMB.seq:*
GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
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US-09-128-142-3

US-09-514-2478-5

US-09-514-2478-5

US-08-917-653-3

US-08-917-653-3

US-08-917-653-3

US-08-255-392-1

US-08-255-392-1

US-08-466-144-3

US-08-466-148-3

US-08-466-148-3

US-08-38-500-3

US-08-38-500-3

US-08-38-500-3

US-08-38-500-3

US-08-38-500-3

US-08-38-500-3

US-08-38-500-3

US-08-38-36-347-7

US-08-668-1288-7

US-08-668-1288-7

US-08-668-1288-7

US-08-905-445-7

                                                                                                                                                                                                                                     number of hits satisfying chosen parameters:
                                                                                                                                                                                                              441362 segs, 153338381 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SUMMARIES
                                                                                                                                                                                                                                                                                                Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                              OM nucleic - nucleic search, using sw model
                                                                                                                                                                        IDENTITY_NUC
Gapop 10.0 , Gapext 1.0
                                                                                                                                                                                                                                                               Minimum DB seq length: 0
Maximum DB seq length: 200000000
                                                                                                                       US-09-765-111A-9
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Match Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Title:
Perfect score:
                                                                                                                                                                           Scoring table:
                                                                                                                                                                                                              Searched:
                                                                                                                                                  Sequence:
                                                                        Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          No.
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Sequence 26, Appl
Sequence 40, Appl
Sequence 2, Appli
Sequence 1, Appli
Sequence 14, Appli
Sequence 6, Appli
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          Sequence 5, Appli
Sequence 5, Appli
Sequence 1068, Appli
Sequence 1068, Appli
Sequence 2, Appli
Sequence 2, Appli
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Appl
Appl
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Sequence 1, Appli
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Sequence 1
Sequence 1
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Patent No. 6200802

GENERAL INFORMATION:
APPLICANT: Blumberg, Bruce
TITLE OF INVENTION: Human Peroxisome Proliferator Activated
TITLE OF INVENTION: Receptor Gamma: Compositions and Method
NORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 61.9%; Score 26; DB 4; Length 1844; Best Local Similarity 85.3%; Pred. No. 0.047; Matches 29; Conservative 0; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: Rockey, Milnamow & Katz, Ltd.
STREET: 2 Prudential Plaza, Suite 4700 180 N. Stetson
US-08-537-002A-5
US-08-683-010-5
US-09-024-4295
US-09-224-1018-1068
US-09-284-970B-65
US-08-981-030-12
US-08-981-030-12
US-08-981-030-12
US-08-981-030-14
US-09-103-840A-2
4 US-09-103-840A-1
US-08-103-840A-1
US-08-103-840A-1
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US-08-103-840A-1
US-08-103-840A-1
US-08-103-840A-1
US-08-103-840A-1
US-08-103-840A-1
US-08-103-840A-1
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APPLICATION NUMBER: US/08/134,557D
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-616-5400
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               25,011
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MOLECULE TYPE: DNA (genomic)
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NAME: Katz, Martin L.
REGISTRATION NUMBER: 25,0
                                                                                             4662 1982 44652 1982 44652 1982 44652 4657 44657 4463765 44657 4463765 44652 5748 11858 14652 5748 11858 14652 5748 11858 14652 5748 11858 14652 5748 11858 14652 5748 11858 14652 5748 11858 14652 5748 11858 14652 5748 11858 14652 5748 11858 14652 5748 11858 14652 5748 11858 14652 5748 11858 14652 5748 11858 14652 5748 11858 14652 14652 14652 14652 14652 14652 14652 14652 14652 14652 14652 14652 14652 14652 14652 14652 14652 14652 14652 14652 14652 14652 14652 14652 14652 14652 14652 14652 14652 14652 14652 14652 14652 14652 14652 14652 14652 14652 14652 14652 14652 14652 14652 14652 14652 14652 14652 14652 14652 14652 14652 14652 14652 14652 14652 14652 14652 14652 14652 14652 14652 14652 14652 14652 14652 14652 14652 14652 14652 14652 14652 14652 14652 14652 14652 14652 14652 14652 14652 14652 14652 14652 14652 14652 14652 14652 14652 14652 14652 14652 14652 14652 14652 14652 14652 14652 14652 14652 14652 14652 14652 14652 14652 14652 14652 14652 14652 14652 14652 14652 14652 14652 14652 14652 14652 14652 14652 14652 14652 14652 14652 14652 14652 14652 14652 14652 14652 14652 14652 14652 14652 14652 14652 14652 14652 14652 14652 14652 14652 14652 14652 14652 14652 14652 14652 14652 14652 14652 14652 14652 14652 14652 14652 14652 14652 14652 14652 14652 14652 14652 14652 14652 14652 14652 14652 14652 14652 14652 14652 14652 14652 14652 14652 14652 14652 14652 14652 14652 14652 14652 14652 14652 14652 14652 14652 14652 14652 14652 14652 14652 14652 14652 14652 14652 14652 14652 14652 14652 14652 14652 14652 14652 14652 14652 14652 14652 14652 14652 14652 14652 14652 14652 14652 14652 14652 14652 14652 14652 14652 14652 14652 14652 14652 14652 14652 14652 14652 14652 14652 14652 14652 14652 14652 14652 14652 14652 14652 14652 14652 14652 14652 14652 14652 14652 14652 14652 14652 14652 14652 14652 14652 14652 14652 14652 14652 14652 14652 14652 14652 14652 14652 14652 14652 14652 14652 14652 14652 14652 14652 14652 14652 14652 14652 14652 14652 14652 14652 14652 14652 14652 14652 14652 14652 14652 14652 14652 1465
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STRANDEDNESS: single
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CITY: Chicago
STATE: IL
COUNTRY: USA
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NAME/KEY:
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US-08-134-557D-1
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Sequence 5, Application US/09514247A

Patent No. 6365361

GENERAL INPORMATION:
GENERAL INPORMATION:
APPLICANT: TANIGUCHI, Tomoyasu
APPLICANT: TANIGUCHI, Tomoyasu
APPLICANT: TANIGUCHI, Tomoyasu
APPLICANT: MIZUKANI, Junko
TITLE OF INVENTION: METHOD FOR IDENTIFYING OR SCREENING AGONIST AND ANTAGONIST TO PP
FILE REFERENCE: TANIGUCHI=6
CURRENT APPLICATION NUMBER: US/09/514,247A
CURRENT APPLICATION NUMBER: PCT/JP98/03734
PRIOR FILING DATE: 1999-08-24
PRIOR FILING DATE: 1999-08-27
PRIOR FILING DATE: 1997-08-27
NUMBER OF SEQ ID NOS: 10
SOFTWARE: PatentIn version 3.0
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                                                                                                                                                               Length 1608;
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Partent No. 6004751

GENERAL INFORMATION:

APPLICANT: Rosenfield, Robert L.

TITLE OF INVENTION: INHIBITORS OF SEBUM FORMATION

TITLE OF INVENTION: INHIBITORS OF SEBUM FORMATION

NUMBER OF SEQUENCES:

ADDRESSEE: Arnold, White & Durkee

STREET: P.O. Box 4433
                                                                                                                                                                                                          0; Indels
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                          Score 23; DB 3;
Pred. No. 0.89;
                                                                                                                                            54.8%; Scor.
100.0%; Pred. No. v...
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                                                                                                                                                                                                                                                20 AGAAATGACCATGGTTGACACAG
                                                                                                                                                          Query Match
Best Local Similarity 100.
Matches 23; Conservative
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                                                                    ; NAME/KEY: CDS
; LOCATION: (91)...(1608)
US-09-484-345-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; LOCATION: (159)..(1679)
US-09-514-247A-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 1679
TYFE: DNA
ORCANISM: Homo sapiens
                             ORGANISM: Homo sapiens
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Matches 23; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CITY: Houston
STATE: Texas
COUNTRY: U.S.
ZIP: 77210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FEATURE:
NAME/KEY: CDS
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US-09-514-247A-5
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US-08-917-653-4
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APPLICANT: Robert McKay
APPLICANT: Alexander H. Borchers
APPLICANT: Alexander H. Borchers
APPLICANT: Brenda F. Baker
TITLE OF INVENTION: ANTISENSE MODULATION OF PEROXISOME PROLIFERATOR-ACTIVATED RECEPTC
FILE REFERENCE: RTS-0104
CURRENT APPLICATION NUMBER: US/09/484,345
CURRENT FILING DATE: 2000-01-18
NUMBER OF SEQ ID NOS: 90
                                                                                                                                                                                        APPLICANT: Smith, Roy G.
TITLE OF INVENTION: ANTIPROLIFERATIVE AGENTS ASSOCIATED WITH
PEROXISOME PROLIFERATOR ACTIVATED RECEPTORS GAMMAI AND GAMM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ô
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0
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                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READBELE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: Power Macintosh 7500/100
                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
ADDRESSEE: Jack L. Tribble
STREET: 126 E. Lincoln Ave., P.O. Box 2000
158 GCCGTGGCCGCAGAATGACCATGGTTGACACG 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: Microsoft Word 6.0
CURRENT APPLICATION DATA:
FILING DATE: 03-Aug-1998
CLASSIFICATION: «URKROWN»
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-09-128-142-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/844,007
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REGISTRATION NUMBER: 32,633
REFERENCE/DOCKET NUMBER: «Ur
TELECOMMONIACTION INFORMATION:
TELEPHONE: (908) 594-4720
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 1518 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                               Sequence 3, Application US/09128142
Patent No. 6294559
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-09-484-345-3
; Sequence 3, Application US/09484345
; Patent No. 6159734
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    20 AGAAATGACCATGGTTGACACAG 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Tribble, Jack L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INFORMATION FOR SEQ ID NO: 3
                                                                                                                                                                                                                                                                                                                                                                           STATE: New Jersey
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                                                                                                                                                                                                                                                                                                                                                CITY: Rahway
                                                                                                                                                                                                                                                                                                                                                                                                  Sn
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 1608
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US-09-128-142-3
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120 AGAAATTACCATGGTTGACACAG 142
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 21.4; DB 3; Length 277; Pred. No. 2.7; 0; Mismatches 1; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     51.0%; Score 21.4; DB 3; Length 373; 95.7%; Pred. No. 3; tive 0; Mismatches 1; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-08-917-653-3

Sequence 3, Application US/08917653

Sequence 3, Application US/08917653

GENERAL INFORMATION:

APPLICANT: Rosenfield, Robert L.

TITLE OF INVENTION: IDENTIFICATION OF ACTIVATORS AND TITLE OF INVENTION: INHIBITORS OF SEGUM FORMATION NUMBER OF SEQUENCES: 4

CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC compatible
CDERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/917,653
FILING DATE: Concurrently Herewith
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APFLICATION NO......
FILING DATE. CONCURRENTLY Herewith CLASSIFICATION: 435
ATORNEY/AGENT INFORMATION:
NAME: Highlander, Steven L. REGISTRATION NUMBER: 37,642
REFERENCE/DOCKET NUMBER: ARCD:216
TELECHONE: (512) 418-3000
TELECHONE: (512) 418-3000
TELEFAX: (512) 418-3000
TELEFAX: (512) 418-7577
INFORMATION FOR SEQ ID NO. 3: SPROMENCE SEQ ID NO. 3: STEURING FOR SEQUENCE FOR SEQ ID NO. 3: STEURING FOR SEQUENCE FOR
                                        APPLICATION NUMBER: US/08/917,653
FILING DATE: Concurrently Herewith
CLASSIFICATION: 435
                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
NAME: Highlander, Steven L.
REGISTRATION NUMBER: 37,642
REFERENCE/DOCKET NUMBER: ACCD:216
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: Arnold, White & Durkee STREET: P.O. Box 4433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   82 AGAAATTACCATGGTTGACACAG 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      20 AGAAATGACCATGGTTGACACAG 42
                                                                                                                                                                                                                                                                                                                                             TELEPHONE: (512) 418-3000
TELEPAX: (512) 447-7577
INFORMATION FOR SEQ 1D NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 277 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   51.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 373 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            22; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
    CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ZIP: 77210
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy o
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; TOPOLOGY: linear
US-08-917-653-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Socal Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Houston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CITY: Houstor STATE: Texas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       22;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-08-917-653-3
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Sequence 1, Application US/0925392

Sequence 1, Application US/0925392

Patent No. 6214850

GENERAL INFORMATION:
APPLICANT: Evans, Ronald M.
APPLICANT: Forman, Barry M.
TITLE OF INVENTION: MODULATORS OF PEROXISOME PROLIFERATOR
TITLE OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pretty, Schroeder, Brueggemann & Clark
STREET: 444 South Flower Street, Suite 2000
                                                                                    APPLICANT: Watson, James D
APPLICANT: Watson, James G
TITLE OF INVENTION: Polymucleotides, polypeptides expressed
TITLE OF INVENTION: by the polymucleotides and methods for their use.
FILE REFERENCE: 11000.103001
CURENT APPLICATION NUMBER: U$/09/724,864
CURENT APPLICATION NUMBER: U$. No. 6380362 60/171,678
PRIOR PILING DATE: 1999-12-23
NUMBER OF SEQ ID NOS: 72
SEQ ID NO 14
LENGTH: 915
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 4; Length 915;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 569 GGGCCAGGATCTCCTGTGAGCAGGCCCCATGGGTGCCCC 531
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 GGGCCAGGCCCTCCTCTCAGAAATGACCATGGTTGACAC 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 51.0%; Score 21.4; Di
Best Local Similarity 71.8%; Pred. No. 3.8;
Matches 28; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REGISTRATION NUMBER: 31,192
REFERENCE/DOCKET NUMBER: P41 9958
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-546-1995
TELEFAX: 619-546-9392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US/09/255,392
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/477,493
FILING DATE:
                 Sequence 14, Application US/09724864
Patent No. 6380362
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INFORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Reiter, Stephen E. REGISTRATION NUMBER: 31,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Los Angeles
CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   USA
                                                                                                                                                                                                                                                                                                                                                                                                                   ; TYPE: DNA
; ORGANISM: Mouse
US-09-724-864-14
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US-09-724-864-14/C
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Gaps

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20 AGAAATGACCATGGTTGACACAG 42

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2005 base pairs

LENGIH:

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334 CCCTTTACTGAAATTACCATGGTTGACACAG 364
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           . Sequence 1, Application US/08465375A; Patent No. 6022897
                                                       Sequence 1, Application US/08477493
Patent No. 5939442
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: 619-546-9392
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2005 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 352..1776
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STRANDEDNESS: both
                                                                                                                                                                                                                                                                                                                  USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: bc
MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                COUNTRY: US
ZIP: 90071
                                                                                                                                                                                                                                                                                                STATE: CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ;
US-08-477-493-1
                                          US-08-477-493-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-08-465-375-1
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Best Local Similarity 80.6%; Pred. No. 4.7;
Matches 25; Conservative 0; Mismatches 6; Indels 0.
                                                                                                                                                                           DB 4; Length 1796;
                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
APPLICANT: EVANS, RONALD M.
APPLICANT: FORMAN, BARRY M.
APPLICANT: OF INVENTION:
APPLICANT: ONG, ESTELITA S.
TITLE OF INVENTION: NOVEL MEMBERS OF THE STEROID/THYROID
TITLE OF INVENTION: SUPERFAMILY AND USES THEREFOR NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE PETENT FOLGOINED #1.25
SOFTWARE PETENT RELEASE #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/484,200
FILING DATE: 07-JUN-1995
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: REITER, STEPHEN E.
REGISTRATION NUMBER: 31,192
REFERENCE/DOCKET NUMBER: 91,197
TELEPHONE: 619-546-1995
TELEPHONE: 619-546-1995
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          B: PRETTY, SCHROEDER, BRUEGGEMANN & CLARK 444 SOUTH FLOWER STREET, SUITE 2000
                                                                                                                                                                         51.0%; Score 21.4; DE nilarity 80.6%; Pred. No. 4.5; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      334 CCCTTTACTGAAATTACCATGGTTGACACAG 364
                                                                                                                                                                                                                                                                               334 CCCTTTACTGAAATTACCATGGTTGACACAG 364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  12 CTCCTCTCAGAATGACCATGGTTGACACAG 42
                                                                                                                                                                                                                                                         12 CTCCTCTCAGAAATGACCATGGTTGACACAG 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                     ; Sequence 1, Application US/08484200 ; Patent No. 5861274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2005 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ZIP: 90071
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy o
                                                                                              CDS
352..1776
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           352..1776
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CITY: LOS ANGELES
STATE: CALIFORNIA
COUNTRY: USA
TYPE: nucleic acid
STRANDEDNESS: both
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      nucleic acid
                                    TOPOLOGY: both
MOLECULE TYPE: cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear MOLECULE TYPE: CDNA
                                                                                                                                                                     Query Match
Best Local Similarity
Matches 25; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; FEATURE:
; NAME/KEY: (
; LOCATION: :
US-08-484-200-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE:
STREET: 44
                                                                                           ; NAME/KEY:
; LOCATION:
US-09-255-392-1
                                                                                                                                                                                                                                                                                                                                                                       US-08-484-200-1
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APPLICANT: Evans, Ronald M.
APPLICANT: Evans, Ronald M.
APPLICANT: Evans, Ronald M.
TITLE OF INVENTION: MODULATORS OF PEROXISOME PROLIFERATOR
TITLE OF INVENTION: ACTIVATED RECEPTOR-GAMMA, AND METHODS FOR THE USE THEREOF
NUMBER OF SEQUENCES.
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pretty, Schroeder, Brueggemann & Clark
STREET: 444 South Flower Street, Suite 2000
CITY: Los Angeles
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
APPLICANT: Evans, Ronald M.
APPLICANT: FORMAN, RONALD M.
TITLE OF INVENTION: SELECTIVE MODULATORS OF PERCXISOME
TITLE OF INVENTION: USE THEREOF
TITLE OF INVENTION: SALK1470-1
CURRENT APPLICATION NUMBER: US/08/465,375A
CURRENT FILING DATE: 1995-06-05
EARLIER APPLICATION DATE: 1995-04-25
NUMBER OF SEQ ID NOS: 7
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                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER EAADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION NOTA:
APPLICATION NUMBER: US/08/477,493
FILING DATE: 07.-UNN-1995
CLASSIFTCATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Relect, Stephen E.
REGISTRATION NUMBER: 31,192
REGISTRATION NUMBER: 31,192
REGISTRATION NUMBER: 91,195
TELECPHONE: 619-546-1995
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APPLICANT Spreader, Cindy A.

TITLE OF INVENTION: CYTOPLASMIC ANTIPROTEINASE-2 AND
TITLE OF INVENTION: CYTOPLASMIC ANTIPROTEINASE-3 AND
CODING SEQUENCES
CORRESPONDENCE: 16
CORRESPONDENCE ADDRESS:
ADDRESSE: Townsend and Townsend Khourie and Crew
STREET: Steuert Street Tower, One Market Plaza
CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              50.0%; Score 21; DB 1; Length 1393; 73.0%; Pred. No. 6.3; tive 0; Mismatches 10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ZIP: 94105-1493
COMPUTER READABLE FORM:
MEDIUM TYPE: Flopy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/385,500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LOCATION: 112..1239
OTHER INFORMATION: /product= "CYTOPLASMIC
OTHER INFORMATION: ANTIPROTEINASE-3 PROTEIN"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     321 ccagrcgcrrcrcacrdaagrgaacaaggcrggcaca 357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5 CCAGGCCCTCCTCAGAAATGACCATGGTTGACACA 41
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/464,148
FILING DATE: 05-UN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 08/385,500
FILING DATE: 08-FEB-1995
ATTORNEY/AGAT INFORMATION:
NAME: Parmelee, Steven W.
REGISTRATION NUMBER: 31,990
REPERDENCE/DOCKET NUMBER: 13952-21
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 467-9600
FILERRAX: (415) 543-5643
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE: CHARACTERISTICS:
LENGTH: 1393 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     13952-21
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; Sequence 3, Application US/08385500
; Patent No. 5712117
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Parmelee, Steven W.
REGISTRATION NUMBER: 31,990
REFERENCE/DOCKET NUMBER: 13:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (206) 467-9600
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INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 1393 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear MOLECULE TYPE: cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         California
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ses 27; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CITY: Sau
STATE: Ca
COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
APPLICANT: EVANS, Ronald
APPLICANT: EVANS, Ronald
APPLICANT: EVANS, Ronald
APPLICANT: EVANS, ROAD,
TITLE OF INVENTION: MODULATORS OF PEROXISOME PROLIFERATOR ACTIVATED RECEPTOR-GAMMA,
TITLE OF INVENTION: AND METHODS FOR THE USE THEREOF
TILE REPREBENCE: SALKI480-2
CURRENT APPLICATION NUMBER: US/09/788,070
CURRENT FILING DATE: 2001-02-16
PRIOR FILING DATE: 1999-02-22
NUMBER OF SEQ ID NOS: 7
SOFTWARE: Patentin version 3.0
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Setent No. 5710026
GENERAL INCORMATION:
GENERAL INCORMATION:
TITLE OF INVENTION: CYTOPLASMIC ANTIPROTEINASE-2 AND
TITLE OF INVENTION: CYTOPLASMIC ANTIPROTEINASE-2 AND
TITLE OF SEQUENCES:
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Khourie and Crew
STREET: Steuart Street Tower, One Market Plaza
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                                                                                                                                                                                                                                  51.0%; Score 21.4; DB 3; Length 2005; 80.6%; Pred. No. 4.7; tive 0; Mismatches 6; Indels 0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 4; Length 2005;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                6; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 51.0%; Score 21.4; D Best Local Similarity 80.6%; Pred. No. 4.7; Matches 25; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                             334 CCCTTTACTGAAATTACCATGGTTGACACAG 364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       334 CCCTTTACTGAATTACCATGGTTGACACAG 364
                                                                                                                                                                                                                                                                                                                                  12 CTCCTCTCAGAAATGACCATGGTTGACACAG 42
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .uence 1, Application US/09788070
ent No. 6413994
                                                                                                                                                                                                                                Query Match
Best Local Similarity 80.6'
Matches 25; Conservative
                                                                                                                 ; FEATURE:
; NAME/KEY: CDS
; LOCATION: (352)...(1776)
US-08-465-375-1
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STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; LOCATION: (352)..(1776)
US-09-788-070-1
                                            LENGTH: 2005
TYPE: DNA
ORGANISM: Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Mus Musculus
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SEQ ID NO 1
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NAME/KEY: CDS
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LENGTH: 2005
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US-09-788-070-1
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APPLICANT: Sprecher, Cindy A.

TITLE OF INVENTION: CYTOPLASMIC ANTIPROTEINASE-2 AND

TITLE OF INVENTION: CYTOPLASMIC ANTIPROTEINASE-3 AND CODING SEQUENCES

NUMBER OF SEQUENCES: 16

CORRESPONDENCE ADDRESS:

ADDRESSEE: Townsend and Townsend Khourie and Crew

STREET: Steuart Street Tower, One Market Plaza

CITY: San Francisco

STATE: California

COUNTRY: US
                                                                                                                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTY:

ZIP: 94105-1493
COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: 1BM PC compatible
COMPUTER: 1BM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentln Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/846,784
FILING DATE: 30-APR-1997
CLASSIFFCATION: 435
PRIOR APPLICATION NUMBER: 08/385,500
FILING DATE: 08-FEB-1995
ATTORNEY/AGENT INPORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LOCATION: 112..1239
COTHER INFORMATION: /product= "CYTOPLASMIC OTHER INFORMATION: ANTIPROTEINASE-3 PROTEIN"
                                                                                                  NAME/KEY: CDS
LOCATION: 112..1239
OCHER INFORMATION: /product= "CYTOPLASMIC
OTHER INFORMATION: ANTIPROTEINASE-3 PROTEIN"
                                                                                                                                                                                                                                                                                                                                                                                                           321 CCAGTCGCTTCTCACTGAAGTGAACAAGGCTGGCACA 357
                                                                                                                                                                                                                                                                                                                                                                          5 CCAGGCCCTCCTCTCAGAATGACCATGGTTGACACA 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Parmele, Steven W.
REGISTRATION NUMBER: 31,990
REPERENCE/DOCKET NUMBER: 13952-21
TELEPHONE: (206) 467-9600
TELEPHONE: (206) 467-9600
TELEPAX: (415) 543-5043
INFORMATION FOR SEQ ID NO: 3: SEQUENCE CHARACTERISTICS:
LENGTH: 139 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 15
US-08-846-784-3
; Sequence 3, Application US/08846784
; Patent No. 5747645
STRANDEDNESS: single
                           TOPOLOGY: linear MOLECULE TYPE: cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear MOLECULE TYPE: cDNA PEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: CDS
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                                                                                  FEATURE:
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321 CCAGTCGCTTCTCACTGAAGTGAACAAGGCTGGCACA 357
                                                                                                       Search completed: January 22, 2003, 00:43:14 Job time: 32.3333 secs
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Gaps 0

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1 cégéccacéccercercasaangaccaregradacaca 42
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: CDS
                                                                                                                                                                                                                                                                                                                                                               US-09-765-111A-9
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US-09-765-111A-3
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                                                                                                                                               LENGTH: 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
Sequence 9, Appli
Sequence 3, Appli
Sequence 22, Appli
Sequence 8, Appli
Sequence 9, Appli
Sequence 1, Appli
Sequence 11, Appli
Sequence 22, Appli
Sequence 5, Appli
Sequence 15, Appli
Sequence 15, Appli
Sequence 15, Appli
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Sequence 990, App
Sequence 109, App
Sequence 36, Appl
Sequence 13, Appl
Sequence 24, Appl
                                                                                       (without alignments)
693.573 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 990,
Sequence 990,
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                                                                                                                                               1 cgggccaggccctcctctca.....aatgaccatggttgacacag
                                                                                                                                                                                                                                                                                                                       Published Applications NA:*

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2: /cgn2_6/ptodata/1/pubpna/PCT7_NEW_PUBLs.seq:*
3: /cgn2_6/ptodata/1/pubpna/USO6_PUBCOMB.seq:*
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                                                                           January 21, 2003, 23:59:20 ; Search time 27 Seconds
          GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
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US-09-765-111A-3
US-09-765-111A-26
US-09-810-107-2212
US-09-816-828-9
US-09-816-828-9
US-09-765-111A-1
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US-09-878-178-990
US-09-925-299-109
US-09-765-111A-13
                                                                                                                                                                                                                        number of hits satisfying chosen parameters:
                                                                                                                                                                                                   393868 seqs, 222934149 residues
                                                                                                                                                                                                                                                                               Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                      OM nucleic - nucleic search, using sw model
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Query
Match Length DB
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Maximum DB seg length: 200000000
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Sequence 2928, Ap
Sequence 4671, Ap
Sequence 1, Appli
Sequence 2411, Ap
Sequence 2410, Ap
Sequence 211, App
Sequence 216, App
Sequence 216, App
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Sequence 1, Appli
Sequence 2893, Ap
Sequence 2893, Ap
Sequence 2893, Ap
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Sequence 9, Application US/09765111A

Patent No. US2002016676A1

GENERAL INFORMATION:

APPLICANT: Fletcher, Jonathan A.

APPLICANT: Fletcher, Jonathan A.

TITLE OF INVENTION: PAX8-PPARgamma NUCLEIC ACID MOLECULES

TITLE OF INVENTION: AND POLYPEPTIDES AND USES THEREOF

TITLE OF INVENTION: AND POLYPEPTIDES AND USES THEREOF

TITLE OF INVENTION: AND POLYPEPTIDES AND USES THEREOF

CURRENT APPLICATION NUMBER: US/09/765,111A

PRIOR APPLICATION NUMBER: US 60/17,109

PRIOR PILLING DATE: 2000-01-20

PRIOR FILLING DATE: 2000-08-14

NUMBER OF SEQ ID NOS: 47

SOFTWARE: FastSEQ for Windows Version 3.0

SECTION OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%; Score 42; DB 10; Length 42; milarity 100.0%; Pred. No. 1.6e-08; Conservative 0; Mismatches 0; Indels
2 US-10-142-373-1

US-09-764-877-2928

US-10-029-17A-1

US-10-029-17A-30

US-09-764-869-2411

US-09-925-301-206

US-09-925-301-206

US-09-946-807-1

US-09-986-907-1

US-09-986-907-1

US-09-867-761-6261

US-09-867-761-885

US-09-867-352-7681
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                                                                            1503841
1503841
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       2005
27483
4484
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551
1506
5470
260
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ORGANISM: Homo Sapiens
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US-09-765-111A-9
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  APPLICANT: Scherf, Uwe
APPLICANT: Gene Logic, Inc.,
TITLE OF INVENTION: Gene Expression Profiles in Liver Cancer;
FILE REPERENCE: 44921-5028-W0
CURRENT APPLICATION NUMBER: US/09/880,107
CURRENT PEPLICATION NUMBER: US 60/211,379
PRIOR FILING DATE: 2001-06-14
PRIOR FILING DATE: 2000-06-14
PRIOR FILING DATE: 2000-06-14
PRIOR FILING DATE: 2000-06-14
PRIOR FILING DATE: 2000-10-02
NUMBER OF SEQ ID NOS: 3950
SOFTWARE: PARENTIN Ver. 2.1
SEQ ID NO 2212
LENGTH: 1811
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: No. U$20020150898A1el Nucleic Acids and TITLE OF INVENTION: Polypeptides
FILE REPRENCE: 791CIPEE
CURRENT APPLICATION NUMBER: U$/09/816,828
CURRENT APPLICATION NUMBER: U$/09/816,828
PRIOR RIJING DATE: 2001-01-26
PRIOR FILING DATE: 2001-01-26
PRIOR FILING DATE: 2001-01-26
PRIOR FILING DATE: 2000-04-18
NUMBER OF SEQ ID NOS: 18
SOFTWARE: PLI_Genes Version 2.0
SEQ ID NO 8
LENGTH: 2260
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 61.9%; Score 26; DB 10; Length 1811; Best Local Similarity 85.3%; Pred. No. 0.17; Matches 29; Conservative 0; Mismatches 5; Indels
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Patent No. US20020150898A1
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APPLICANT: Tang, Y. Tom
APPLICANT: Zhou, Ping
APPLICANT: Goodrich, Ryle
APPLICANT: Asundi, Vinod
APPLICANT: Ren, Peiyan
APPLICANT: Nen, Peiyan
APPLICANT: Nen, Peiyan
APPLICANT: Nen, Piong J.
APPLICANT: Wang, Zhiwei
PPLICANT: Zhang, Jie
PPLICANT: Zhang, Jie
PPLICANT: Hang, Jien-Rui
PPLICANT: Hang, Jien-Rui
PPLICANT: Hang, Jien-Rui
PLICANT: Denmanac, Radoje T.
TLE OF INVENTION: No. DESSORT
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US-09-816-828-8/c
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Sequence 26, Application US/09765111A;
GENERAL INFORMATION:
APPLICANT: Fletcher, Jonathan A.
APPLICANT: Fletcher, Jonathan A.
TITLE OF INVENTION: PAX8-PPARGamma NUCLEIC ACID MOLECULES;
TITLE OF INVENTION: PAX8-PPARGamma NUCLEIC ACID MOLECULES;
TITLE OF INVENTION: AND POLYZEPTIDES AND USES THEREOF;
CURRENT APPLICATION NUMBER: US/09/765,111A;
CURRENT APPLICATION NUMBER: US 60/177,109
PRIOR FILING DATE: 2000-01-20
PRIOR FILING DATE: 2000-01-20
PRIOR FILING DATE: 2000-01-20
PRIOR FILING DATE: 2000-01-20
PRIOR FILING DATE: 2000-01-30
PRIOR FILING DATE: 2000-01-30
SOFTWARE: FastSEQ for Windows Version 3.0
SOFTWARE: FastSEQ for Windows Version 3.0
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APPLICANT: Kroll, Todd G.
TITLE OF INVENTION: PAX8-PPARGamma NUCLEIC ACID MOLECULES
TITLE OF INVENTION: AND POLYPEPTIDES AND USES THEREOF
FILE REFERENCE: BO801/7196/ERP/MAT
CURRENT APPLICATION NUMBER: US/09/765,111A
CURRENT FILING DATE: 2001-01-18
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                                                                                                               CUKKENT FILING DATE: 20019/765,111A

PRIOR APPLICATION NUMBER: US 60/177,109

PRIOR FILING DATE: 2000-01-20

PRIOR PILING DATE: 2000-014

PRIOR PILING DATE: 2000-08-14

NUMBER OF SEQ ID NOS: 47

SOFTWARE: FastSEQ for Windows Version 3.0

SEQ ID NO 3

LENGTH: 2553
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; Sequence 2212, Application US/0980107; Patent No. US20020142981A1
; GENERAL INFORMATION:
; APPLICANT: Horne, Darci T.
; APPLICANT: Vockley, Joseph G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61.9%; ;
milarity 85.3%; I
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US-09-765-111A-26
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Matches 29; Conserv
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Best Local Similarity
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; NAME/KEY: CDS
; LOCATION: (1).
US-09-765-111A-3
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US-09-765-111A-26
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                                          60.0%; Score 25.2; DB 10; Length 42; ilarity 78.9%; Pred. No. 0.14; Conservative 0; Mismatches 8; Indels
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APPLICANT: Fletcher, Jonathan A.
APPLICANT: Fletcher, Jonathan A.
APPLICANT: Fletcher, Jonathan A.
APPLICANT: Fretcher, Jonathan A.
TITLE OF INVENTION: PAXG-PPARgamma NUCLEIC ACID MOLECULES:
TITLE OF INVENTION: AND POLYPEPTIDES AND USES THEREOF;
FILE REFERENCE: BO801/7196/FRP/MAT.
CURRENY FILING APPLICATION NUMBER: US/09/765,111A
CURRENY FILING DATE: 2000-01-20
PRIOR PLING DATE: 2000-01-20
PRIOR FILING DATE: 2000-01-20
PRIOR FILING DATE: 2000-01-3
PRIOR FILING DATE: 2000-08-14
NUMBER OF SEQ ID NOS: 47
NUMBER: FastSEQ for Windows Version 3.0
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APPLICANT: Fletcher, Jonathan A.
APPLICANT: Reall, Todd G.
TITLE OF INVENTION: PAX8-PRESTABRAMM NUCLEIC ACID MOLECULES
TITLE OF INVENTION: PAX8-PRESTABRA
TITLE OF INVENTION: AND POLYPEPTIDES AND USES THEREOF
FILE REPERENCE: B0801/7196/ERP/MAT
CURRENT APPLICATION NUMBER: US/09/765,111A
CURRENT FILING DATE: 2000-10-18
PRIOR APPLICATION NUMBER: US 60/177,109
PRIOR FILING DATE: 2000-01-20
PRIOR FILING DATE: 2000-08-14
NUMBER OF SEQ ID NOS: 47
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1 Similarity 78.9%; Pred. No. 0.38;
30; Conservative 0; Mismatches 8;
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; Sequence 11, Application US/09765111A
; Patent No. US20020106796A1
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ORGANISM: Homo Sapiens
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ORGANISM: Homo Sapiens
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Matches 30; Conserva
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; LOCATION: (3)...(41)
US-09-765-111A-11
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US-09-765-111A-7
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APPLICANT: Fletcher, Jouathan A.
APPLICANT: Fletcher, Jouathan A.
APPLICANT: Fletcher, Jouathan A.
APPLICANT: Kroll, Todd G.
ITILE OF INVENTION: PAX8 PPARgamma NUCLEIC ACID MOLECULES
ITILE OF INVENTION: AND POLYPEPTIDES AND USES THEREOF
FILE REPRENENCE: B0801/7196/ERP/MAT
CURRENT APPLICATION NUMBER: US/09/765,111A
CURRENT FILING DATE: 2000-01-18
PRIOR APPLICATION NUMBER: US 60/177,109
PRIOR APPLICATION NUMBER: US 60/225,079
PRIOR FILING DATE: 2000-08-14
NUMBER OF SEQ ID NOS: 47
SEQ ID NOS: 47
LENGTH: 42
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                                                                                 Sequence 9, Application US/09816828
Patent No. US20020150898A1
                                                                                                                                                                Zhou, Ping
Goodrich, Ryle
Asundi, Vinod
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Xue, Aidong J.
Ma, Yunqing
Wang, Zhiwei
Zhao, Qing A.
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Wang, Jian-Rui
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; LOCATION: (1612)..(2211)
US-09-816-828-9
                                                                                                                                            APPLICANT: Tang, Y. Tom
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ORGANISM: Homo sapiens
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ORGANISM: Homo Sapiens
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NAME/KEY: CDS
LOCATION: (3)...(41)
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                                                          JS-09-816-828-9/c
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58.1%; Score 24.4; DB 10; Length 42; 82.4%; Pred. No. 0.3;
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; Sequence 5, Application US/09765111A
; Sequence 6, Application US/09765111A
; GENERAL INFORMATION:
APPLICANT: Elector, Jonathan A.
APPLICANT: Erol, Todd G.
TITLE OF INVENTION: PAR8-PPARgamma NUCLEIC ACID MOLECULES
; TITLE OF INVENTION: PAR8-PPARGamma NUCLEIC ACID MOLECULES
; TITLE OF INVENTION: PAR8-PPARGamma NUCLEIC ACID MOLECULES
; TITLE OF INVENTION: PAR8-PPARGamma NUCLEIC ACID MOLECULES
; TITLE OF INVENTION: PAR8-PPARGamma NUCLEIC ACID MOLECULES
; TITLE OF INVENTION: PAR8-PPARGamma NUMBER: US/08/765,111A
; CURRENT FILING DATE: 2000-01-18
; PRIOR FILING DATE: 2000-01-18
; NUMBER OF SEO ID NOS: 47
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 5
; LEMCTH: 2625
                                                 Indels
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Sequence 22, Application US/09765111A
Patent No. US20020106796A1
GENERAL INFORMATION:
APPLICANT: Fletcher, Jonathan A.
APPLICANT: Kroll, Todd C.
TITLE OF INVENTION: PAX8-PPARgamma NUCLEIC ACID MOLECULES
TITLE OF INVENTION: AND POLYPEPTIDES AND USES THEREOF
FILE REFERENCE: B0801/7196/ERP/MAT
CURRENT APPLICATION NUMBER: US/09/765,111A
CURRENT FILING DATE: 2001-01-18
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Pred. No. 0.83;
0; Mismatches 6;
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PRIOR APPLICATION NUMBER: US 60/177,109
PRIOR FILING DATE: 2000-01-20
PRIOR APPLICATION NUMBER: US 60/225,079
PRIOR PLING DATE: 2000-08-14
NUMBER OF SEQ ID NOS: 47
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 22
LENGTH: 2596
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       58.1%;
82.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 82.47
Matches 28; Conservative
                                            28; Conservative
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US-09-765-111A-22
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FEATURE:
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US-09-765-111A-5
Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FEATURE:
NAME/KEY: CDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 11
US-09-765-111A-5
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APPLICANT: TANABE SITYAKU CO. LTD.
APPLICANT: TANABE SITYAKU CO. LTD.
APPLICANT: TANIGUCHI, TOMOYASU
APPLICANT: TANIGUCHI, TOMOYASU
TITLE OF INVENTION: METHOD FOR IDENTIFYING OR SCREENING AGONIST AND
TITLE OF INVENTION: ANTAGONIST TO PPAR
FILE REPERENCE: TANIGUCH=6
CURRENT APPLICATION NUMBER: US/10/109,886
CURRENT PILING DATE: 2002-04-01
PRIOR FILING DATE: 2000-02-28
PRIOR FILING DATE: 1998-08-24
PRIOR FILING DATE: 1998-08-24
PRIOR RELING DATE: 1997-08-27
NUMBER OF SEQ ID NOS: 10
SOFTWARE: PATENTIN VESSION 3.0
                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ( ; Gaps
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                     Length 2625;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INPORMATION:
APPLICANT: Fletcher, Jonathan A.
APPLICANT: Fletcher, Jonathan A.
APPLICANT: Fletcher, Jonathan A.
TITLE OF INVENTION: PAX8-PPARgamma NUCLEIC ACID MOLECULES;
TITLE OF INVENTION: PAX8-PPARgamma NUCLEIC ACID MOLECULES;
TITLE OF INVENTION: AND POLYPEPTIDES AND USES THEREOF;
CURRENT ENDOR: BO800/7196/ERP/MAT.
CURRENT APPLICATION NUMBER: US/09/765,111A
CURRENT APPLICATION NUMBER: US 60/177,109
PRIOR FILING DATE: 2000-01-20
PRIOR FILING DATE: 2000-01-30
SEQ ID NOS: 47
SOFTWARE: ESEUSEQ for Windows Version 3.0
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                                                                                                                           Indels
Ouery Match 58.1%; Score 24.4; DB 10; Best Local Similarity 82.4%; Pred, No. 0.84; Matches 28; Conservative 0; Mismatches 5;
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                                                                                                                                                                                                                 9 GCCCTCCTCAGAAATGACCATGGTTGACACAG 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; Sequence 15, Application US/09765111A; Patent No. US20020106796A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-10-109-886-5; Application US/10109886; Patent No. US20020119499A1
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LOCATION: (159)..(1679)
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ORGANISM: Homo sapiens
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Matches 23; Conserv
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US-10-109-886-5

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                                                                                                                                                                                                             Sequence 990, Application US/10046935;
Patent No. US20020156011A1;
GENERAL INFORMATION:
APPLICANT: Jargy, Yuqiu
APPLICANT: Barlocker, Susan L.
APPLICANT: Secriet, Heather
APPLICANT: Wang, Aljun
JLCANT: WICLE, John A.
FLE REPERENCE: 210121.52701
FILE REPERENCE: 210121.52701
CURRENT APPLICATION NUMBER: US/10/046,935
CURRENT APPLICATION NUMBER: US/10/046,935
NUMBER OF SEQ ID NOS: 2239
NUMBER: PSEC ID NOS: 2239
SOFTWARE: FSEC ID NOS: 2239
SOFTWARE: FSEC ID NOS: 2339
LENTH: 343
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US-09-878-178-990

Sequence 990, Application US/09878178

Patent No. US2002017552A1

Patent No. US2002017552A1

Patent No. US2002017552A1

PLICANT: Janag, Yuqiu

PLICANT: Harlocker, Susan L.

APPLICANT: Harlocker, Susan L.

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY

TITLE OF INVENTION: AND DIAGNOSIS OF COLON CANCER

FILE REFERENCE: 210121,527

CURRENT APPLICATION NUMBER: US/09/878,178

NUMBER OF SEQ ID NOS: 2237

SOFTWARE: PastSEQ for Windows Version 4.0

SEQ ID NO 990

LENGTH: 343

TYPE: DNA

NOGANISM: Homo sapien

US-09-878-178-990
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  54.8%; Score 23; DB 12; Length 1679; 100.0%; Pred. No. 2.8; tive 0; Mismatches 0; Indels (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 52.4%; Score 22; DB 9; Length 343; Best Local Similarity 100.0%; Pred. No. 4.9; Matches 22; Conservative 0; Mismatches 0; Indels
                                                 0; Indels
                                                                                                                       239 AGAAATGACCATGGTTGACACAG 261
                                                                                             20 AGAAATGACCATGGTTGACACAG 42
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Query Match
Best Local Similarity 100.(
Matches 23; Conservative
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Best Local Similarity 100.0
Matches 22, Conservative
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CORGANISM: Homo sapiens
US-10-046-935-990
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US-10-046-935-990
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121 GAAATGACCATGGTTGACACAG 142

21 GAAATGACCATGGTTGACACAG 42

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Search completed: January 22, 2003, 02:09:58 Job time : 31 secs
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/tissue_type="placenta"
/note="Vector: pCMVSPORT 6; Site_1: Not1; ist strand cDNA
was primed with a Not1-oligo(dT) primer. Five prime end
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Homo sapiens"
/db_xref="taxon:9606"
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ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DEFINITION
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JOURNAL
COMMENT
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AL543579
LOCUS
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KEYWORDS
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AQ150638 HS 3197 B
BM924484 AGENCOURT
BI091883 602858760
BI820841 603034063
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677.725 Million cell updates/sec
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                                                                January 21, 2003, 23:02:45; Search time 1003.67 Seconds
                                                                                                                                     1 cgggccaggccctcctca.....aatgaccatggttgacacag 42
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GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                          16154066 segs, 8097743376 residues
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                                        OM nucleic - nucleic search, using sw model
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Gapop 10.0 , Gapext 1.0
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BE684416 187639 MA AQ586497 RPCI-11-4
BI682587 463715 MA BM28446 524715 MA AQ729636 HS 2162 B AW653703 102525 MA BIS35582 399198 MA BIS35582 399198 MA BIS35582 399198 MA BIS35582 S99198 MA
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BH105865 RPCT-24-2
BL455326 B1455326
B1547966 60189375
BE865554 601677894
H49473 yq89c04.rl
H5367 yq86f08.rl
AAO153612 zl73f06.r
AAO1689 ze21f02.s
AAI14023 EST185877
BG569798 602590418
AZB83149 RPCT-23-2
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BG183368 RST2262 A
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AIS56679 UI-R-C2p-
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BM790089 K.EST0069
BM74007 K.EST0017
AW954935 EST366905
AZ25817 RPCI-23-1
BE867033 601442867
BE373645 601226035
AAS50301 1430m3 gm
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BE227998 894036F09
BE724296 894073G03
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Euheria, Primates, Catarrhini, Hominidae, Homo.
1 (bases 1 to 903)
Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
Full-length cDNA libraries and normalization
Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                AL543579 GTI_NFL006_PL2 Homo sapiens cDNA clone CS0D1006Y110 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: segref@genoscope.cns.fr, Web : www.genoscope.cns.fr.
                                                                                                                                                                                                                                                                                                                            ALIGNMENTS
                                                                                                                         BIO81730
BIB950167
BHI05865
BJ455326
BIS47966
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BA65554
H54473
H53507
               AJ274160
BG183368
BF546300
AIS56679
                                             BQ199668
BE900105
BE685416
BE684603
AQ586497
BI682587
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AW653703
BI535582
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BM790089
BM744007
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AA010869
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BG569798
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AA550301
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AL543579.1 GI:12876058
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72 GCCGTGGCCGCAGAATGACCATGGTTGACACAG 105
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AQ150638.1 GI:3544096
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/note="Organ: pooled brain, lung, testis; Vector: pcwv-Sporrd, Site_1: hor!; Site_2: hosh (destroyed); RNA source anonymous pool of male brains, age range 23-27; l male lung, age 27; and 1 male testis, age 69. Library is oligo-dr primed and directionally cloned (BcoRV site is oligo-dr primed and directionally cloned (BcoRV site is oligo-dr primed and directionally cloned (BcoRV site is ninsert size range 1-3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 021. Note: this a NIH MGC Library."
enriched, double-stranded cDNA was digested with Not I and cloned into the Not I and Eco RV sites of the pCVVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies. Contact: Feng Liang Life Technologies, a division of Invitrogen 9800 Medical Center Drive Rockville, Maryland 20850, USA Fax: (1) 301 610 8371 Email: filiang@lifetech.com URL: http://fullneigth.invitrogen.com"
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-6707162 NIH_MGC_115 Homo sapiens cDNA clone IMAGE:5754203
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1141)
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Tissue Procurement: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://fmage.lnl.gov
Plate: LLAM12791 row: d column: 12
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National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
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Pred. No. 18;
0; Mismatches 5; Indels C
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2.
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Pred. No. 17;
0; Mismatches
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Location/Qualifiers
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BM922116
BM922116.1 GI:19372495
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1 Similarity 85.3%;
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5', mRNA sequence.
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AQ150638 432 bp DNA linear GSS 08-0CT-199 HS_3197_B1_F01_MR CIT Approved Human Genomic Sperm Library D Homo sap:ens genomic clone Plate=3197 Col=1 Row=L, DNA sequence.
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Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
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                                                                                                                                                                                                                                                                                           1 (bases 1 to 432)
Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T.,
Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D.
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|Colone="Plate=3197 Col=1 Row=L"
|Colone lib="CIT Approved Human Genomic Sperm Library D"
|Sex="male
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: Mahairas GG, Wallace JC, Hood L
High Throughput Sequencing Center
University of Washington
401 Queen Anne Avenue North, Seattle, WA 98109, USA
Tel: (206) 616-3818
Fax: (206) 616-382
Email: Jwallace@u washington.edu
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Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
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/cell_line="MGC36"
/lab_host="DH10B"
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622858760F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:5000102 5',
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 730)
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LiNL at:
http://incge.llnl.gov
plate: LLAM12808 row: i column: 01
High quality sequence start: 95
High quality sequence start: 95
High quality sequence store: 480.
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Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LINL at:
http://mage.lnl.gov
Plate: LiAM11031 row: 9 column: 15
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National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
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Pred. No. 1.1e+02;
0; Mismatches 0; Indels (
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100.0%; Pred. No. 1...
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/clone="IMAGE:5760840"
/clone_lib="NIH_MGC_116"
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/db_xref="taxon:9606"
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Location/Qualifiers
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/clone_lib="NIH_MGC_10"
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Tissue Procurement: ATCC
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                                                                                                                                                                                                                                                                                                                                         /lab host="DH10B"
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BI091883
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TITLE
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COMMENT
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/db xref="traxon:gept=1.0"
/db xref="traxon:gept=1.0"
/clone="NMAGE:5175351"
/clone="NHAGE:5175351"
/clone="NHAGE:5175351"
/clone="NHAGE:5175351"
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pCWV-SPORF6; Site 1: Noti; Site 2: EcoRV (destroyed); RNA source anonymous pool of 6 male brains, age range 23-27; and lung, age 27; and 1 male testis, age 69. Library is oligo-dT primed and directionally cloned (EcoRV site is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.8 kb, insert size range 1-3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code.
021. Note: this is a NIH_MGC Library."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BI820841 901 bp mRNA linear EST 04-0CT-2001
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0
/note="Organ: cervix; Vector: pCMV-SPORT6; Site_1: Not1; Site_2: Sal1; Cloned unidirectionally, Primer: Oligo dT. Average insert size 1.5 kb. Library prepared by Life Technologies."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bukaryofa; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.

1 (base; 1 to 901)

NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
Plate: LLAM1436 row: m column: 16
High quality sequence stop: 876.
                                                                                                                                                                                                                                                                         Gaps
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0
                                                                                                                                                                                                         54.8%; Score 23; DB 13; Length 730;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                54.8%; Score 23; DB 13; Length 901; 100.0%; Pred. No. 2.3e+02;
                                                                                                                                                                                                                                                                   10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
                                                                                                                                                                                                                                                                                                                                                                    708 GGGCTAGACCCTCATCTCAGAAACTAGCAGAGTTGGGAC 670
                                                                                                                                                                                                                                                                                                                       2 GGGCCAGGCCCTCCTCAGAAATGACCATGGTTGACAC 40
                                                                                                                                                                                                                                 Pred. No. 2.2e+02;
                                                                                                                      206 t
                                                                                                                                                                                                                                                                0; Mismatches
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/organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Robert Strausberg, Ph.D.
                                                                                                             171 g
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BI820841.1 GI:15932391
                                                                                                                                                                                                                                 74.48;
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DEFINITION

RESULT 7 BE227998

ACCESSION VERSION

ORGANISM

KEYWORDS SOURCE

AUTHORS

TITLE

REFERENCE

JOURNAL

COMMENT

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/note="Vector: pBluescript II SK-; Site_1: EcoRI, Site_2.

Xhol; This library, constructed by John Davies and Jeffr.

MoDermott, combines cDNAs from CC-1690 cells grown to

mid-log phase in TAP (acetate-containing) medium in the
light, TAP medium in the dark, HS (minimal) medium in the
light, TAP medium in the dark, HS (minimal) medium in
ambient levels of CO2 and HS medium bubbled with 5% CO2.

PolyA mRNA was purified from each sample, pooled and cDNA
Sypthesized. The CDNA was directionally cloned into lambda
ZAP II (Extragene) in the EcoRI (s') and Xhol (s') sites.

PBRUESCRIPT II SK- plasmids were excised from the lambda
ZAP clones by superinfection with ExAssist (Stratagene)
phage. The library was normalized using method 4 described
in Bonaldo et al 1996) Genome Research 6: 791-806."
McDermott, J. P., Silflow, C., Stern, D. and Surzycki, R.
Analyses of the Chlamydomonas reinhardtii Genome: A Model,
Unicellular System for Analyzing Gene Function and Regulation in
Vascular Plants; project phase 2
L Unpublished (2000)
CONTECT: Charles Hauser
DOMB Box 91000
Duke University
Durham, NC 27708-1000
Tel: 919 613 8159
Fax: 919 613 8177
Email: chauser@duke.edu.
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/db xref="taxon.5530"
/dlone="Ma#1795"
/clone lib="whetarhizium anisopliae ARSEF 2575"
/note="Vector: UniZap; Metarhizium anisopliae was grown on
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /clone_lib="C. reinhardtii CC-1690, normalized, Lambda Zap
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota, Fungi, Ascomycota, Pezizomycotina, Sordariomycetes,
Hypocreales, Clavicipitaceae, mitosporic Clavicipitaceae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         54.3%; Score 22.8; DB 12; Length 469; 79.4%; Pred. No. 2.2e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Chlamydomonas reinhardtii"
                                                                                                                                                                                                                                                                                                                                                                                                                                               /strain="CC-1690 wild type mt+ 21gr"
/db xref="taxon:3055"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Metarhizium anisopliae"
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                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
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Screen, S.E., Mathur, P. and
EST analysis of the insect
Unpublished (1999)
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AUTHORS
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KEYWORDS
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                                                                                                                                                      COMMENT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Anote="Vector: pBluescript II SK-; Site_1: BCORI, Site_2: Xhol; This library. Constructed by John Davies and Jeffrey McDermoct, combines CDNAs from CC-1690 cells grown to mid-log phase in TAP (acetate-containing) medium in the light, TAP medium in the dark, HS (minimal) medium in ambient levels of CO2 and HS medium bubbled with 5% CO2. PolyA mRNA was purified from each sample, pooled and cDNA synthesized. The cDNA was directionally cloned into lambda ZAP II (Extragene) in the BCORI (S') and XhoI (3') sites. pBluescript II SK- plasmids were excised from the lambda ZAP clones by superinfection with ExAssist (Stratagene) phage. The library was normalized using method 4 described in Bonaldo et al 11996) Genome Research 6: 791-8066."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               409 DP MRNA linear EST 14-SEP-2000 Chlamydomonas reinhardtii CC-1690, normalized, Lambda Zap II Chlamydomonas reinhardtii cDNA, mRŅA Sequence.
                                                                                     BE227998 361 bp mRNA linear EST 06-JUL-2000 894036F09.x1 C. reinhardtii CC-1690, normalized, Lambda Zap II Chlamydomonas reinhardtii cDNA, mRNA sequence.
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Chlamydomonas reinhardtii
Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;
Chlamydomonadaceae; Chlamydomonas.
                                                                                                                                                                                                                                                                                                                                                                                  1 (bases 1 to 361)
Grossman, A., Davies, J., Federspiel, N., Harris, E., Lefebvre, P.,
McDermott, J. P., Silflow, C., Stern, D. and Surzycki, R.
Analyses of the Chlamydomonas reinhardtii Genome: A Model,
Unicellular System for Analyzing Gene Function and Regulation in
Vascular Plants; project phase 2
Unpublished (2000)
Contact: Elizabeth H. Harris
DOMB BOX 91000
                                                                                                                                                                                                                                                                                                  Chlamydomonas reinhardtii
Eukaryota, Viridiplantae, Chlorophyta, Chlorophyceae, Volvocales,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 (bases 1 to 469)
Grossman,A., Davies,J., Federspiel,N., Harris,E., Lefebvre,P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /strain="CC-1690 wild type mt+ 21gr"
/db_xref="taxon:3055"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 10;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              90 GGGCATGGCCTCCCTAAGAAATGCCCACGGTT 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                          Chlamydomonadaceae; Chlamydomonas.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: chlamy@duke.edu.
Location/Qualifiers
1. .361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            27708-1000, USA
                                                                                                                                                                                                                                                                       Chlamydomonas reinhardtii.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BE724296.1 GI:10125592
                                                                                                                                                                                                       BE227998.1 GI:8933237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity 79.4 tes 27; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Tel: 919 613 8164
Fax: 919 613 8177
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88

BASE COUNT ORIGIN

Query Match

Matches

Best

LOCUS DEFINITION

BE724296

RESULT 8

q ò

ACCESSION VERSION KEYWORDS SOURCE ORGANISM

REFERENCE

Durham, NC

source

FEATURES

Euteleostomi;

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/strain="sprague-Dawley"
/db xref="taxon:0116"
/clone="UI-R-C2p-rj-c-02-0-UI"
/clone="UI-R-C2p-rj-c-02-0-UI"
/clone="UI-R-C2p-rg-c-02-0-UI"
/dev stage="adult"
/lab_host="DH10B (Life Technologies)"
/lab_host="DH10B (Life Technologies)"
/lab_host="DH10B (Life Technologies)"
/lab_host="DH10B (Life Technologies)"
/lab_host="UI-R-C2p
library; as subtracted library derived from the UI-R-C1
library, which is a subtracted library derived from the UI-R-C1
library, which is a subtracted library consisted of a
mixture of individually tagged normalized libraries
constructed from xat placenta, adult lung, brain, liver,
kidney, heart, spleen, ovary, muscle, 8, 12 and 18-day
embryo. The tag is a string of 3-5 nucleotides present
between the Not I site and the oligo-dT track which allows
identification of the library of origin of a clone within
the mixture. The subtracted library (UI-R-C2p) was
constructed as follows: PCR amplified oDNA inserts from
UI-R-C1 clones from which 3' ESTS had been derived was
used as a driver in a hybridization with the UI-R-C1
library in the form of single-stranded circles. The
remaining single-stranded circles (subtracted library) was
purified by hydroxyapatite column chromatography,
converted to double-stranded circles and electroporated
library in the Stranded circles and electroporate the
UI-R-C2D library which procedure has been accommended to double the page of the pag
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: msoares@blue.weeg.uiowa.edu

CDNA Library Preparation: M.B. Soares Lab Clone distribution:

clones will be available through Research Genetics (www.resgen.com)

This clone is also available through the I.M.A.G.E. Consortium at

LLNL (info@inage.llni.gov). IMAGE ID= 1789869
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AIS56679 453 bp mRNA linear EST 05-JUL-1999 UI-R-C2p-rj-c-02-0-UI.sl UI-R-C2p Rattus norvegicus cDNA clone UI-R-C2p-rj-c-02-0-UI 3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    UI-R-C2p library. This procedure has been previous, described (Bonaldo, Lennon and Soares, Genome Research 6:
                                                                                                                                                                                                                  Bonaldo,M.F., Lennon,G. and Soares,M.B.
Normalization and subtraction: two approaches to facilitate gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                   451 Eckstein Medical Research Building Iowa City, IA 52242, USA
                                                                                                Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleost
Mammalia; Eutheria, Rodentia, Sciurognathi, Muridae, Murinae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     53.8%; Score 22.6; DB 12; Length 433; 75.7%; Pred. No. 2.5e+02;
                                                                                                                                                                                                                                                                                                                                                               Contact: Soares, MB
Program for Rat Gene Discovery and Mapping
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    285 GGGCCAGCTCCTCGGCTCAGACTGATCATTACTGAC 249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        organism="Rattus norvegicus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GGGCCAGGCCCTCCTCAGAAATGACCATGGTTGAC 38
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76 c 1
                                                                                                                                                                                    (bases 1 to 433)
                                                                                                                                                                                                                                                                                                                                                                                                                        University of Iowa
                                          Norway rat.
Rattus norvegicus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Tel: 319 335 8250
Fax: 319 335 9565
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Best Local Similarity
                                                                                                                                                                                                                                                                              discovery
                                                                                                                                                                                                                                                                                                                                    97044477
                                                                                                                                                                  Rattus.
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                                                                     ORGANISM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 (bases) to remain the following the following the following the farming on, J., Sherf B., Rundlett, S., Jackson, P.D., Perry, R., Cain, S., Leventhal, C., Thornton, M., Ramachandran, R., Whittington, J., Lerner, L., Costanzo, D., McElligott, K., Boozer, S., Mays, R., Smith, E., Veloso, N., Klika, A., Hess, J., Cothren, R., Lo, K., Offenbacher, J., Danzig, J. and Ducar, M. Cothren, R., Lo, K., Offenbacher Creation of genome-wide protein expression libraries using random activation of gene expression
1227151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0
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insect cuticle for 24 hours. A cDNA library was constructed in the unidirectional Lambda vector, UniZap" 1 228 c 189 g 97 t 1 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /db_xref=""axon:9606"
/clone lib="Athersys RAGB Library"
/cell line="HT1080"
/note="See 'Creation of Genome-wide Protein Expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                            BG183368
RST2262 Athersys RAGE Library Homo sapiens cDNA, mRNA sequence.
                                                                                                                                                                                                               Gaps
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Pred. No. 2.6e+02;
0; Mismatches 12; Indels 0;
                                                                                                                                                      Length 633;
                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                               183 cccascadoccorcoradocaadacadagiroccada 224
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                                                                                                                                                                                                                                                            1 CGGGCCAGGCCCTCCTCAGAAATGACCATGGTTGACACAG 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3201 Carnegie Ave, Cleveland, OH 44115, USA
Tel: 216 431 9900
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                                                                                                                                                      DB 9;
                                                                                                                                                Score 22.8; DB 9;
Pred. No. 2.5e+02;
0; Mismatches 12
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Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BG183368.1 GI:13705055
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Scott J. Cain
Athersys, Inc.
                                                                                                                                                54.3%;
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1 Similarity 71.4%;
30; Conservative
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                                                                                                                                                                        Similarity
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Best Local
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BF546300/c
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2 GGGCCAGGCCCTCTCTCAGAATGACCATGGTTGAC 38
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                                                                                                                                                                                                                                                                                                                                                                  Rattus norvegicus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Tel: 319 335 8250
Fax: 319 335 9565
                                                                                                                                                                                                                                                     BQ199668.1
                                                                                                                                                                                                                                                                                                                                Norway rat.
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KEYWORDS
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/clone="U1-R-C2p-r" c-02-0-U1"
/clone="U1-R-C2p-r" c-02-0-U1"
/clone="U1-R-C2p-r" c-02-0-U1"
/dev stage="adula" c.p.
/dev stage="adula" c.p.
/dev stage="wall" c.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: mscares@blue.weeg.ulowa.edu
The sequence tag present in the CDNA between the NotI site and the oligo-dr track served to identify it as a clone from the normalized adult Spleen library. CDNA Library Preparation: M. Failma Bonaldo, Ph.D. Clone distribution: clones will be available through Research Genetics (www.resgen.com) This clone is also available through the I.M.A.G.E. Consortium at LiML (info@image.lln.gov). IMAGE
ID=1789869 The following repetitive elements were found in this Seg primer: MI3 Forward
POLYA=No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        remaining single-stranded circles (subtracted library) was
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ô
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                                                                                                                                       Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               converted to double-stranded circles and electroporated
                                                                                                                                                                                                                                                 1 (bases 1 to 453)
Bonaldo,M.F., Lennon,G. and Soares,M.B.
Normalization and subtraction: two approaches to facilitate gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Soares, MB
Program for Rat Gene Discovery and Mapping
University of Iowa
451 Eckstein Medical Research Building Iowa City, IA 52242, USA
Fat: 319 335 9250
Fax: 319 335 9565
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             purified by hydroxyapatite column chromatography,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2 GGGCCAGGCCCTCCTCAGAAATGACCATGGTTGAC 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            'organism="Rattus norvegicus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 123 t
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                                                                                                                                                                                                                                                                                                                                                                                         Genome Res. 6 (9), 791-806 (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               791-806, 1996)"
82 c 8
AI556679.1 GI:4489042
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                                                                                                             Rattus norvegicus
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Matches 28; Conserv
                                                                       Norway rat
                                                                                                                                                                                                                                                                                                                                                                  discovery
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                                                                                                                                                                                                                       Rattus.
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ORIGIN
                                                                                                             ORGANISM
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                                                                                                                                                                                                                                                                                           AUTHORS
TITLE
                                                                                                                                                                                                                                                         REFERENCE
       VERSION
KEYWORDS
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348 GGGCCAGCTCCTCGGCTCAGAACTGATCATTACTGAC 384

g ò

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The sequence contained an oligo-dr track that was present in the oligonuclectide that was used to prime the synthesis of first strand cDNA and therefore this may represent a bonafide poly A tail. The sequence tag present in the cDNA between the NoII site and the oligo-dr track served to verify it as a clone from the normalized rat cell line R337-5a library cDNA Library Preparation. M.B. Scarse Lab Clone distribution: clones will be available through Research Genetics (www.resgen.com) The following repetitive elements were found in this CDNA sequence: 1-38,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             the Not I cloning site and dT18 stretch. The Rat Cell Line R3327-5A was provided by Mary Hendrix of the University of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ·.
             EST 02-MAY-2002
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (Normalization and Subtraction: Two Approaches to Facilitate Gene Discovery. Genome Research 6: 791-806, 1996). The oligonucleotide used to prime first strand synthesis contained the sequence tag GGACTAGATC between
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 (bases 1 to 737)
Bonaldo,M.F., Lennon,G. and Soares,M.B.
Normalization and subtraction: two approaches to facilizate gene
BQ199668
UI-R-DQ1-clh-k-13-0-UI.sl UI-R-DQ1 Rattus norvegicus cDNA clone
UI-R-DQ1-clh-k-13-0-UI 3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                451 Eckstein Medical Research Building Iowa City, IA 52242, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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TAG_SEQ=GGACTAGATC"
169 c 126 g 209 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Soares, MB Program for Rat Gene Discovery and Mapping
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/db_xref="taxon:10116"
/clone="UI-R-DQ1-clh-k-13-0-UI"
/clone_lib="UI-R-DQ1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: msoares@blue.weeg.uiowa.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Genome Res. 6 (9), 791-806 (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
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Seg primer: M13 Forward
                                                                                                                                                                                                                                                         GI:20416133
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g

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Email: smith@email.marc.usda.gov
Single pass sequencing. Bases called and alt trimmed with phred
v.980904.e. Vector identified by cross_match with the -minscore 18
PCR PRimers
.G.L., Heaton,M.P., Laegreid,W.W., Rohrer,G.A., Chitko-McKown,C.G., Pertea,G., Holt,I., Karamycheva,S., Liang,F., Quackenbush,J. and
                                                                                Sequence evaluation of four pooled-tissue normalized bovine cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /db_xref="taxon:9913"
/cloane_lib="makec_480v"
/lissue_type="pooled"
/lab_host="DH10B"
/note="vector: pCMV SPORT6; Site_1: Not1; Site_2: Sal1;
/library made_from pooled_tissue_from_day_20 and_day_40
embryos."
                                                                                                         libraries and construction of a gene index for cattle Genome Res. 11 (4), 626-630 (2001)
                                                                                                                                                                                 Contact: Smith TPL USDA, ARS, US Meat Animal Research Center USDA, ARS, US Meat Animal Research Center Po Dox 166, Clay Center, NE 68933-0166, USA Tel: 402 762 4366 Pax: 402 762 4390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 22.4; DB 10;
Pred. No. 2.7e+02;
0; Mismatches 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3 GGCCAGGCCCTCTCTCAGAATGACCATGGTTGACACAG 42
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Job time : 1006.67 secs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Bos taurus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Plate: 100 row: P column: 9 Seg primer: ATTTAGGTGACACTATAG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       FORWARD: AGGAAACAGCTATGACCAT
BACKWARD: GTTTTCCCAGTCACGACG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
1.309
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Best Local Similarity 72.5%;
Matches 29; Conservative C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     65 G
                                                       Keele, J.W.
                                                                                                                                                                21180013
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ORIGIN
                                                                                                                                    JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FEATURES
                                                                                                                                                                                            COMMENT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             //organism="Homo sapiens"
/organism="Homo sapiens"
/db xref="taxon:8606"
/clone='unaxon:8606"
/clone='unaxon:8606"
/clone='unaxon:8606"
/clone='ub="MIH WAGC 21"
/tissue_type="choriocarcinoma"
/tab_hose='nH10B (phage-resistant)"
/note='uorgan: placenta; Vector: pOTB7; Site_1: XhoI;
Site_2: BCoRI; cDNA made by oligo-dT priming.
Site_2: BCoRI; cDNA made by oligo-dT priming.
Directionally cloned into EcoRIXAnol sites using the
following 5' adaptor: GGCAGAGGG. Size-selected >500bp
for average insert size 1.8kb. Library constructed by
Ling Hong in the laboratory of Gerald M. Rubian (University
of California, Berkeley) using Zab-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)."
                                                                                                                                  BE900105 860 bp mRNA linear EST 29-SEP-2000 601673007F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3956136 5',
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EST 25-APR-2001
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Bos taurus

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Butheria; Cecartiodactyla; Ruminantia; Pecora; Bovoidea;

Bovidae; Bovinae; Bos.

1 (Dases 1 to 309)

Smith, T.P. L., Grosse, W.M., Freking, B.A., Roberts, A.J., Stone, R.T.,

Casas, E., Wray, J.E., White, J., Cho, J., Fahrenkrug, S.C., Bennett
                                                                                                                                                                                                                                                                                                                        Homo sapiens
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia; Butheria, Primates, Catarrhini, Hominidae, Homo.
1 (bases 1 to 860)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: cgapbs-r@mail.nfh.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
Plate: LLCM831 row: m column: 01
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .,
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29 2.3 54.8 144815 2 ANUZ230.2 ANUZ230.2 2 3 54.8 144815 2 ANUZ230.2 ANUZ230.2 2 3 54.8 144815 2 AC19459 3 2 2.8 54.8 146749 2 AC097171 3 22.8 54.3 17937 9 AC016683 AC09943 3 22.8 54.3 10185 1 AE009474 AC09943 3 22.8 54.3 10685 9 AC09025 AC00943 3 22.8 54.3 126497 9 AC09025 AC0	7 23. 55.7 19477	ACTO/8	07836 MUS II
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33 22.8 54.8 179937 9 ACU16683 ACU3717 ACU3717 9 ACU16683 ACU3717 9 ACU16683 ACU3717 9 ACU16683 ACU3717 9 ACU16683 ACU3717 9 A	29 23 54.8 11481 20 22 54.8 14634	ACLEVA	4, 6
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5 22.6 53.8 1765 9 AY048695 AY048695 Mac	5 22.6 53.8 176	AY0486	Y048695 Ma

RESULT 1	
HSPPARGAM	
LOCUS	HSPPARGAM 1766 bp mRNA linear PRI 21-AUG-1997
DEFINITION	H.sapiens mRNA for peroxisome proliferactor activated receptor
	gamma.
ACCESSION	X90563
VERSION	X90563.1 GI:1480099
KEYWORDS	peroxisome proliferator-activated receptor gamma.
SOURCE	Homo sapiens.
ORGANISM	Homo sapiens
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
	Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
REFERENCE	1 (bases 1 to 1766)
AUTHORS	Lambe, K.G. and Tugwood, J.D.
TITIE	A human beroxisome-proliferator-activated receptor-damma is

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5 CGCAGGCATGGTGGCAGAATGACCATGGTTGACACAG 42
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/note="h ppar gamma gene"
173. .1606
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Gene Expr. 4 (4-5), 281-299 (1995)
95307078
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/db_xref="taxon:9606"
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YDSYIKSFPLTKAKARAILTGKTTDKSPFVIYDMSLAMMEDKIKFKHTPLQEQSKE
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LSCDRPGLLNVKFIEDIQDNLLQALECQLKLNHPESSQLFAKLLQKMTDLRQIVTEHV
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DGVILSEGOCFWITREFLKSLRKSPROPORPKREFAVKFNALELDDSDLAFITAVILLS
GDRPGLLNVKPIEDIQDNLLQALELQLKLNHPBSSQLFAKLLQKMTDLRQIVTEHVQL
LQVIKKTETDMSLHPLLQEIYKDLY"
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Homo sapiens peroxisome proliferator activated receptor gamma
(PPARG) mRNA, complete cds.
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SLMAI ECRVCGDKASGFHYGVHACEGCKGFFRRTIRLKLI YDRCDLNCRIHKKSRNKC
                                                                                                                                                         Submitted (07-AUG-1995) K.G. Lambe, Zeneca Central Toxicology Lab., Alderley Park, Macclesfield, Cheshire SK10 4TJ, UK Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ISTPHYEDI PFTRTDPVVADYKYDLKLOGYOSA I KVEPAS PPYYSEKTOLYNKPHEEP
SNSLMA I ECRVCGDKASG PHYGVHA CEGCKGFFRRTI RLKLI YDRCDLNCR I HKKSRN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         translation="MTMVDTEMPFWPTNFGISSVDLSVMEDHSHSFDIKPFTTVDFSS"
activated by inducers of adipogenesis, including thiazolidinedione
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Matches 33; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                          Qi.J.S., Dead.-Yajnik, V., Greene, M.E., Raaka, B.M. and Samuels, H.H. The ligand-binding domains of the thyroid hormone/retinoid receptor gene subfamily function in vivo to mediate heterodimerization, gene silencing, and transactivation Mol. Cell. Biol. 15 (3), 1817-1825 (1995)
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Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammallai, Butheria, Primates, Catarrhini, Hominidae, Homo.

1 (Dases 1 to 1808)
Greene, M.E., Blumberg, B., McBride, O.W., Yi, H.F., Kronquist, K., Kwan, K., Hsieh, L., Greene, G. and Nimer, S.D.
Isolation of the human peroxisome proliferator activated receptor gamma cDNA: expression in hematopoietic cells and chromosomal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Direct Submission
Submitted (26-DEC-2001) University of Chicago, Chicago, IL 60637,
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/product="peroxisome proliferator activated receptor
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4 (bases 1 to 1808)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence update by submitter
On Dec 26, 2001 this sequence version replaced gi:722619.
Location/Qualifiers
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dev_stage="adult"
1. .I808
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86.8%; Pred. No. 0.45;
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/db_xref="GI:20905690"
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MTVLGTLPMFLFPVYWLIRDLLLLGAYIVAWALFFLTARRYACVRCINFECPVNRVSV
GVKEEFKKRDGFPGNIEVSKEEFWAAGSGRCTSLRVKHEFKDFLYWNFVTLTILFSAG
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RPHPPGKFDIAITSLGFMILIFPFLFFLLEIPFLLGTYLVSISVFLLTIWRYECGRCI
YFECPFNRVPAEVRKEFEKKDPERMILK"
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LAILLSGFVITTAVPLKLQYYYIAEYYRNTVCNNCGKEFICRETEKPDIKEISTPETY
                                                                                                                                                                       Martinez-Arias,R., Henne,A., Wiezer,A., Baeumer,S., Jacobi,C., Brueggemann,H., Lienard,T., Christmann,A., Boemecke,M., Steckel,S., Bhattacharyya,A., Lykidis,A., Overbeek,R., Klenk,H.-P., Gunsalus,R.P., Fritz,H.-J. and Gottschalk,G.
The genome of Methanosarcina mazei: Evidence for lateral gene transfer between Bacteria and Archaea
                                                                                                                                                                                                                                                                                              June 1 December 1 December 1 December 2 (bases 1 to 14697)

Deppenmener, U., Johann, A., Hartsch, T., Merkl, R., Schmitz, R.A., Martinez-Arias, R., Henne, A., Wiezer, A., Baeumer, S., Jacobi, C., Brueggemann, H., Lienard, T., Christmann, A., Boemecke, M., Steckel, S., Bhattacharyya, A., Lykidis, A., Overbeek, R., Klenk, H.-P., Steckel, S., Gunsalus, R.P., Fritz, H.-J. and Gottschalk, G.
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DIRVSKEQETMERRYYRCKLCNYEDIAATEFPMVFDSGGVSAIEWNIDYEDYFG"
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VREFTRQLKENTDKDIMLVGGSQLIKAFLEEDLVDDMIVFIVPIILGGGIPLFDRIGK
EIKLKMTNTERYESGLLRTEYNLKPT"
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Direct Submission Submitted (12-2001) Goettingen Genomics Laboratory, Institute For Miorobiology and Genetics, Grisebachstrasse 8, Goettingen 37077, Germany
                                                                                                                               1 (bases 1 to 14697)
Deppenmeier,U., Johann,A., Hartsch,T., Merkl,R., Schmitz,R.A.
                                                                                     Archaea; Buryarchaeota; Methanococci; Methanosarcinales; Methanosarcinaceae; Methanosarcina.
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/protein_id="AAM30929.1"
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/transl_table=11
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/db_xref="taxon:192952"
complement(444. .1532)
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/db_xref="G1:20905692"
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Methanosarcina mazei Goel
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Methanosarcina mazei strain Goel, section 136 of 379 of the
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                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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1 (bases 1 to 1844)
1 (bases 1 to 1844)
Human perversione proliferator activated receptor gamma: compositions and methods
Patent: US 6200802-A 1 13-MAR-2001;
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86.8%; Pred. No. 0.45;
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/note="EMBL/GenBank Accession No. L40904"
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Sequence 2212 from Patent WO0229103.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Homo sapiens"
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433 c 421 q
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AE013354 AE008384
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1 CCATCGCAGGCATGGTGGCAGAAATGACCATGGTTGACAC
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/db_xref="G1:20905699"
                                                                                                                                complement (9519. .11231)
                                                                                    complement (9519. .11231)
                                                                                                                                                                                                                                                           /protein_id="AAM30936.
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/db_xref="GI:20905700"
                                                                                                                                                    /gene="MM1240"
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AP005513.1 GI:21728115
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                                                                                                                                                                                             /codon_start=1
/transl_table=:
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ilarity 80.0%;
Conservative (
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SYNYSDKTAV VLKYYRAKEVSPARA-PNLHRIVDGLVWKAGIPKPKYYIVGSGMPPARFATG
RDPKHAAVAATTGILELLSYEEMEGVILAHELAHVKNRDILISAIAATLAGVVTMLAHM
AQWAAIFGGFGGRDDGSGIVGLIAVAIVAFIAATLIQLAISRSEREFAADEEGARIS
RKPWALADALEKLEYGNSHYRARVSDVQAKESSAHWFIVNPLKGGAVQSLFRTHPVTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /translation="MEIKCRCGDKCIKPVSEVLKDIELFYKPCRDCKTEKIRKFSPLA
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KCSPAFFEELVVYLTKMGYGGSRVDAGKAIGKSHOOGIDGIIKEDRIGLDVIYIQAR
RWEGTVSKPEIQKPAGALIGKKAKKGVFITTSSFSKEAIEYADFTGNIVLVDGEMLAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FMDLMVVIENPYTDRIPADTAMNEERLEEYAKQLISGENIQDFEYTYGGRLRNMNGEV
DQIEYVIEKLKESPISRRATAVTWIPPVDTKVNEVPCMILDDFKIRDEKVHLTTLFRS
HDFGGAYPANLYGLSKLLEYVAEKVGVEPGVITTVSISAHVYDHDWDMVENIVKGIN"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /trānslation="MRASISKSSIKGEVFAPPSKSYTHRAITLAALSKESIIHRPLLS
ADTLATIRASEMFGAAVRREKENLIIQGSNGKPGIPDDVIDAANSGTTLRFMTAIAGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FIIPGKQKYDLKQYTVPGDFSSASYLLAAAAMLEGSBITVKNLFPSKQGDKVIIDTLK
QMGADITWDMEAGIVTVRGGRKLKAITFDAGSTPDLVPTVAVLASVAEGTSRIBNAEH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VRYKETDRLHALATELPKMGVSLKEEMDSLTITGGTLEGAEVHGWDDHRIVMSLAIAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                'translation="MENKFEIGRIIRAKNISDAWYRGLNIIWNHGRVITDERGSQIKE
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protein_id="AAM30933.1"
db_xref="G1:20905695"
                                                                                                                                                                                                                                                                                    LMIEYNVGVSRVKSYEVKKMDTDYFEDGVI"
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/product="methyltransferase"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             /product="protease HTPX"
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/EC_number="2.1.1.45"
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/transl_table=11
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                                                                                                                                                                                                                                                                                                                                                                                                number="3.4.24.-"
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/g768. .Rnf.
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/gene="MM1237"
6011. .6664
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                                                                                                                                                                                                                                                                                                         4612. .5475
/gene="MM1236"
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/gene="MM1236"
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/codon_start=1
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/transl_table=
note="MM1235"
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BQINLDBIDNRFGNCKCGKRQLDIVMAHVLKVMIDBGIKDKKANLRNACVPLITPGYL
TDYVPELPENSIVILSERMNECABRVIKRYPBVKGVLKGDARKTVGIKDSDSSPHIY
BELJAGCDLRCDIIQPPQALGIYKVPHEHIBFPQVHSPKIBILBKALKDYNDPSVLD
CTCCSPGSLGITCLKAGARKVVFNDIWHPALBTTLINLBANGFPVKFSGSEKELIASGN
NFBVYSTDIRELVNYLDBKYDICIVDTFPGVDTAKFIBAAGKLCKNVVVI"
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SYMSGGVGFTQYATAAYTDDILDNNTYYDVDYINDKYNGAANLGTDNKVKATLDVVKL
IATESTLYGIETYEKFPTALEDHFGGSQRATVLAAASGVACALATGNANAGLSGWYLS
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GHSVRLQEDGVMFDMLDRRRLEGSTIIMDKDQVAIPLDRKVDLGKPMSSEEAAKRTTI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        QEMNVETHPALVDDCYVKVFTGDDELADEIDKQYVININKMFS3EQAAQIKASMGKTT
WQAIHIPTIVSRTTDGAQTSRWAAMQIGMSFISAYAMCAGEAAVADLSFAAKHAAL
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AGIAQAAHSGRGDAFTVNPLIKVCFADDLMPFNFAEPRREFGRGAIREFVPAGERSLI
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Bukaryota; Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AP005513 . 155438 bp DNA linear HTG 11-JUL-20
Oryza sativa (japonica cultivar-group) chromosome 2 clone
OSJUBBa0014E22, *** SEQUENCING IN PROGRESS ***, in ordered pieces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Oryza satīva (japonica cultivar-group) (cultivar:Nipponbare) DNA, clone:OSJNBaO014E22.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /codon start=1
/transl_table=11
/product="Methyl-coenzyme M reductase, gamma subunit"
                                                                                                                                                                                                                                                                                                                                                                                                                                                   /transI_table=11
/product="Methyl-coenzyme M reductase, alpha subunit"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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are based on estimates that have provided by the submitter. This sequence will be replaced by the finished sequence as soon as it is available and the accession number will be preserved.

* NOTE: This is a 'working draft' sequence.

* This sequence will be replaced

* by the finished sequence as soon as it is available and

* the accession number will be preserved.
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/product="peroxisome proliferator activated receptor gamma
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Blbrecht, A., Chen, Y., Cullinan, C.A., Hayes, N., Leibowitz, M.D., Moller, D.E. and Berger, T. Cullinan, C.A., Hayes, N., Leibowitz, M.D., Molecular cloning, expression and characterization of human peroxisome proliferator activated receptors gamma 1 and gamma 2 Biochem. Biophys. Res. Commun. (1996) In press
2 (bases 1 to 1518)
Elbrecht, A., Chen, Y., Cullinan, C.A., Hayes, N., Leibowitz, M.D., Moller, D.B. and Berger, J.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HSU63415 Deroxisome proliferato activated receptor gamma 2 mRNA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                    /organism="Oryza sativa (japonica cultivar-group)"
/cultivar="Nipponbare"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 2; Length 185387;
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/db_xref="taxon:9606"
/cell_type="fat_cell"
                                                                                                                                                                                                                                                                                                                                            /db_xref="taxon:39947"
/chromosome="2"
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                                                                                                                                                                                                                               Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                             /clone="P0010C01"
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                                                                                                                                                                                                                                                        Submitted (10-JUL-2002) Takuji Sasaki, National Institute of Agrobiological Sciences, Rice Genome Research Program, Kannondai 2-1-2, Tsukuba, Ibaraki 305-8602, Japan (2-1-2, Tsukuba, Ibaraki 305-8602, Japan (2-1-2, Tsukuba, Ibaraki 305-8602, Japan (2-1-2) Religious Safficiacia (2-1-2) Religious Safficiacia (2-1-2) Religious Safficiacia (2-1-2) Religious Safficiacia (2-1-2) Religious Safficiacia (2-1-2) Religious Safficiacia (2-1-2) Religious Safficiacia (2-1-2) Religious Safficiacia (2-1-2) Religious Safficiacia (2-1-2) Religious Safficiacia (2-1-2) Religious Safficiacia (2-1-2) Religious Safficiacia (2-1-2) Religious Safficiacia (2-1-2) Religious Safficiacia (2-1-2) Religious Safficiacia (2-1-2) Religious Safficiacia (2-1-2) Religious Safficiacia (2-1-2) Religious Safficiacia (2-1-2) Religious Safficiacia (2-1-2) Religious Safficiacia (2-1-2) Religious Safficiacia (2-1-2) Religious Safficiacia (2-1-2) Religious Safficiacia (2-1-2) Religious Safficia (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (20-FEB-2002) Takuji Sasaki, National Institute of Agrobiological Sciences, Rice Genome Research Program; Kannondai 2-1-2, Tsukuba, Ibaraki 305-8602, Japan (E-mail:tsasaki@nias.affrc.go.jp, URL:http://rgp.dna.affrc.go.jp, Tel:81-298-38-7441, Fax:81-298-38-7468)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NOTE: It currently consists of 1 contigs. Gaps between the contigs are represented as runs of N. The order of the pieces is believed to be correct as given, however the sizes of the gaps between them
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Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta; Magnollophyta, Liliopsida; Poales, Poaceae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Oryza satīva (japonica cultivar-group) (cultivar:Nipponbare) DNA, clone:P0010C01.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                    Sasaki,T., Matsumoto,T. and Katayose,Y.
Oryza sativa nipponbare(GA3) genomic DNA, chromosome 2, BAC
clone:OSUNBABONO11E2
Published Only in Database (2002)
2 (bases 1 to 155438)
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Oryza sativa nipponbare(GA3) genomic DNA, chromosome 2, PAC
clone:P0010C01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                organism="Oryza sativa (japonica cultivar-group)'
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* This sequence will be replaced

* by the finished sequence as soon as it is available and

* the accession number will be preserved.
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                                                                                                                                                                                                             Sasaki, T., Matsumoto, T. and Katayose, Y. Direct Submission
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2 (bases 1 to 185387)
Sasaki,T., Matsumoto,T. and Yamamoto,K.
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80.6%; Pred. No. 53;
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chromosome="2"
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Ehrhartoideae; Oryzeae; Oryza.
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Best Local Similarity
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QSAIKVEPASPPYYSEKTOLYNKPHEEPSNSIAAIECRVCGDKASGFHYGVHACEGCK
GFFRRTIRLKLIYDRCDINCRIHKKSRNKCQYCRFQKCLAVGMSHNAIRFGRMPQAEK
EKLLAEISSDIDQLNPESADLRALAKHLYDSYIKSFPLTKAKARAILTGKTTDKSPFV
IYDMNSLMMGEDKIKFKHITPLQEQSKEVAIRIFQGCQFRSVEAVQEITEYAKSIPGF
                                                                                                                                                                                                        VNLDLNDQVTLLKXGVHEITYTMLASLANKDGVLISBGOGFMTREFLKSIRKPFGDFM
BPKFBFAVKFNALELDDSDLAIFIAVIILSGDRPGLLNVKPIEDIGDNLLQALELQLK
LAHPBSSQLFAKLLQKMTDLRQIVTEHVQLLQVIKKTETDMSLHPLLQEIYKDLY"
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                                                                                                 /tränslation="MGETLGDSPIDPESDSFTDTLSANISQEMTMVDTEMPFWPTNFC
ISSVDLSVMEDHSHSFDIKPFTTVDFSSISTPHYEDIPFTRTDPVVADYKYDLKLQEY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Unclassified.

1 (bases 1 to 1679)
Taniguchi,T. and Mizukami,J.
Method for identifying or screening agonist and antagonist to PPAR
Patent: US 636536 A 5 02-APR-2002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.

    (bases 1 to 1679)

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                              /product="ligand activated transcription factor PPARgamma2"
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D93231. GI:1199768
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                                                                                                                                                                                                                                                                                                                       57.6%; Score 24.2; DB 9; 78.4%; Pred. No. 83;
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                                                                                                                                                                                                                                                                                                                                                                                                                              157 GCAAACATATCACAAGAAATGACCATGGTTGACACAG 193
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Sequence 5 from patent US 6365361.
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Homo sapiens adipose cDNA to mRNA.
Homo sapiens
                                                               /protein_id="AAC51248.1"
/db_xref="GI:1711117"
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405 c 377 g
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           /codon_start=1
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J. Biol. Chem. 272 (12), 8071-8076 (1997)
                                                                                                                                                                                                                                                                                                                                                                   McKay,R., Borchers,A.H. and Baker,B.F. Antisense modulation of peroxisome proliferator-activated receptor
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1 (bases 1 to 1608)
Mukherjee,R.; Jow,L.; Croston,G.E. and Paterniti,J.R. Jr.
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Mukherjee,R., Jow,L., Croston,G.E. and Paterniti,J.R. Jr.
Direct Submission
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     DB 9; Length 1518;
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 ; Score 24.2; DB
; Pred. No. 83;
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Patent: US 6159734-A 3 12-DEC-2000;
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Pred. No. 83;
                                                                                                                                                                                                  Sequence 3 from patent US 6159734.
AR121467.1 GI:14105043
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/db xref="taxon:966"
/fissue_type="heart"
91. .1608
/note="nuclear receptor"
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1 Similarity 78.4%;
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VIYDMNSLAMGEDKIKRYHITPLQEQSKEVALRIPGGCQRSVBAVDETTEYAKSIPG
FVINDLNDQVTLLKYGVHEIIYTMLASLANKDGVLISEGGGFMTREFLKSLRKPRDF
MERKERFANKFWALELDDSDLAIFIAVILLGGBRRQLLAVWFIEDIQNNLLQALELQL
KLNHPESSQLFAKLLQKMTDLRQIVTEHVQLLQVIKKTETDMSLHPLLQEIYKDLY
Submitted (29-JAN-1996) Shigeaki Kato, Tokyo University of Agriculture, Department of Agricultural Chemistry; Sakuragaoka 11-1, Setagaya-ku, Tokyo 156, Japan (E-mail:ktake@m.u-tokyo.ac.jp, Tel:03-5477-2318, Fast:03-5477-2619)
On or before Mar 17, 1999 this sequence version replaced gi:2077947, gi:1197807.
D83136: Submitted (18-Jan-1996).
                                                                                                                                                                                                                                                                                                                                                                                   ISSVDLSVMEDHSHSFDIKPFTTVDFSSISTPHYEDIPFTTDPVVADYKYDLKLGEY
QSAIKVEPASPPYYSEKTQLYNKPHEEPSNSLMAIECRVCGDKASGFHYGVHACEGCK
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Mammalia; Butheria, Primates, Catarrhini; Hominidae, Homo.
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No coding mutations are detected in the peroxisome proliferator-activated receptor-gene in Japanese patients with lipoatrophic diabetes
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/db_xref="taxon:9606"
/tissue_type="adipose"
159. .1679
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/protein_id="BAA18949.1"
/db_xref="GI:1945622"
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/db_xref="taxon:9606"
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<115. .340
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1 Similarity 78.4%;
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                                                                                          COMMENT
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Eukaryofa, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.

El (basea I to 13567)

Bao,J., Bao,Q., Bao,W., Bian,X., Cao,T., Chen,C., Chen,J., Ding,H., Dong,W., Fan,H., Feng,X., Gong,J., Guan,Q., Gu,X., Guo,D., Guo,Z., He,L., Hu,S., Huang,F., Jin,Y., Kang,N., Li,C., Li,C., Li,F., Li,J., Li,J., Li,J., Liu,Y., Liu,N., Liu,B., Liu,Y., Li,J., Liu,Y., Liu,N., Liu,B., Liu,Y., Li,J., Liu,Y., Liu,N., Liu,B., Liu,Y., Li,J., Liu,Y., Liu,J., Liu,B., Liu,B., Liu,Y., Li,J., Wang,J., Wang,J., Wang,J., Wang,J., Wang,J., Wang,J., Wang,X., Wang,X., Wang,X., Wang,Y., Zhang,Y., Zhang,H., Zhang
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                                                                                                                                                                                                                                                                                                                 Gaps
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Homo sapiens chromosome 3 clone RP11-167M22 map 3p, complete
                                                                                                                                                                                                                                                                                                            0
                                                                                                                                                                                                                Length 416;
                                                                                                                                                                                                                                                                                                            0; Indels
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Chemistry: Dye-terminator: ET 55% of reads
Chemistry: Dye-terminator Big Dye; 45% of reads
Chemistry: Dye-terminator Big Dye; 45% of reads
Chemistry: Program: Phrap; version 0.990329
Consensus quality: 586 bases at least Q40
'note="ppar gamma common exonl"
                                                                                                                                                                                                                57.1%; Score 24; DB 9; 100.0%; Pred. No. 97;
                                                                                                                                                                                                                                       100.0%; Prea. ....
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Center clone name: RP11-167M22
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http://www.genomics.org.cn
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            110 CAGAAATGACCATGGTTGACACAG 133
                                                                                   67
                                                                                                                                                                                                                                                                                                                                                                                                19 CAGAAATGACCATGGTTGACACAG 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AC093174.1 GI:15148930
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Signature of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the contro
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Wu,O., Bao,J., Bao,W., Bian,X., Cao,T., Chen,C., Chen,J.,
Wu,Q., Bao,J., Bao,W., Feng,X., Gong,J., Guan,Q., Gu,X., Guo,D.,
Ding,H., Dong,W., Fan,H., Feng,X., Gong,J., Guan,Q., Gu,X., Guo,D.,
Li,F., Li,G., Li,J., Li,L., Li,S., Li,T., Liu,Y., Liu,N., Li,W.,
Li,W., Li,W., Li,W., Li,W., Li,Y., Liu,Y., Liu,Y., Liu,B.,
Liu,Y., Li,W., Li,W., Li,W., Li,Y., Liu,Y., Liu,B.,
Song,S., Sun,M., Sun,Y., Lan,X., To,X., Wang,X., Wang,X.,
Wang,J., Wang,J., Wang,L., Wang,L., Wang,R., Wang,X., Wang,X.,
Wang,Y., Wang,J., Xie,F., Xian,Z., Xie,Y., Yan,C., Yang,X., Yu,B.,
Zhang,X., Zhang,H., Zhang,H., Zhang,L., Zhang,M.,
Yu,J. and Yang,H., Zhang,Y., Zhang,Z., Zhu,B., Zhu,N.,
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Homo sapiens chromosome 3 clone RP11-30G23 map 3p, complete
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On Mar 20, 2001 this sequence version replaced gi:8072582
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                                                                                                                                     1.48x in Q20 bases; sum-of-contigs
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Consensus quality: 919 bases at least Q30 consensus quality: 1154 bases at least Q20 Insert size: 1198; sum-of-contigs Quality coverage: 1.48x in Q20 bases;sum-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        26554 g 42494 t
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Unpublished
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/chromosome="3"
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http://www.genomics.org.cn
Contact:hgc@igtp.ac.cn
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25375 c 26554 q 4
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AC090947.1 GI:13384351
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Best Local Similarity 100.0
Matches 24, Conservative
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KEYWORDS
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                                                                                                                                                                                                        Consensus quality: 499 bases at least Q40 consensus quality: 605 bases at least Q30 Consensus quality: 674 bases at least Q20 Insert size: 692; sum-of-contigs Quality coverage: 2.80x in Q20 bases;sum-of-contigs
                                                                                                 Sequencing vector: pUC18; 100% of reads
Chemistry: Dye-terminator: ET 55% of reads
Chemistry: Dye-terminator Big Dye; 45% of reads
Assembly program: Phrap; version 0.990329
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.----- Project Information
                                                Center clone name: RP11-30G23
                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="3"
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Job time : 898.333 secs
                Center project name:1% project
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Matches 24; Conserve
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Human PPARgamma cD Human PPARgamma co Human PPARgamma co Peroxisome prolife

Human PAX8e8-PPARG

Human PPAR gamma P

Body weight gain : Propionibacterium

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Peroxisome prolife Human cDNA differe

Human cancer relat Human cancer relat

Human colon tumour Human colon cancer

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PAX8-PPARgammal; oncogene; cytostatic; PAX8; PPARgammal; cancer;
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AAS44653
AAH76285
AAH76282
AAD21022
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AAZ57563
AAH26111
AAH42011
AAH42011
AAS59593
AAX59593
AAX16672
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AAT35333
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AAF81676
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AAV21207
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14-AUG-2000; 2000US-0225079.
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1936
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Copyright (c) 1993 - 2003 Compugen Ltd.
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Result

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Mouse PPAR-gamma A Human type IV coll DNA encoding human Type IV collagen N Human alpha2(IV)NC

Drosophila melanog Drosophila melanog Drosophila melanog Bovine PPAR coding

Rat PPAR-gamma A/B

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                                                                                                                                                                                                                                                                                                                                                                      subject having a disorder characterized by the presence of a PAX8-PPARgammal, where the disorder is cancer, e.g. follicular carcinoma. The PAX8-PPARgammal molecules are also useful for providing nucleotide and amino acid sequences useful for detecting the above disease. The present sequence represents the nucleotide sequence including and surrounding the fusion juncture in the PAX8e9-PPARgammael DNA.
                                                                                                                                                                                                                                                                              contains a PAX8 coding region fused to PPARgammal coding region. The PAX8-PPARgammal polypeptides can be expressed by standard recombinant methodology. A PPARgamma ligand or agent is useful for treating a
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                                                                                       New PAX8-PPARc1 oncogene and oncoprotein, useful for detecting and treating certain tumors or cancers, e.g. follicular carcinoma
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Mismatches
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                                                                                                                                                                                      Claim 21; Page 119; 145pp; English.
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Matches 42; Conservative
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P-PSDB; AAB85801.
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methodology. A PPARgamma ligand or agent is useful for treating a subject having a disorder characterized by the presence of a PAX8-PPARgamma1, where the disorder is cancer, e.g. follioular carcinoma. The PAX8-PPARgamma1 molecules are also useful for providing nucleotide and amino acid sequences useful for detecting the above disease. The present sequence represents a human PAX8e9(-exon 8)-PPARgammae1
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                                                                                                                                                                                                                                                                                                                                Sequence 2596 BP; 660 A; 745 C; 672 G; 519 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1140 CCATCGCAGGCATGCTGGCAGAATGACCATGGTTGACACAG 1181
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                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%; Score 42; DB 22; 100.0%; Pred. No. 3.4e-07;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 CCATCGCAGGCATGGTGGCAGAAATGACCATGGTTGACACAG
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1..2625
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14-AUG-2000; 2000US-0225079
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Length 2625;

DB 22;

Score 42;

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The invention relates to an oncogene designated PAX8-PPARgammal that contains a PAX8 coding region fused to PPARgammal coding region. The PAX8-PPARgammal polypeptides can be expressed by standard recombinant methodology. A PPARgammal ligand or agent is useful for treating a subject having a disorder characterized by the presence of a PAX8-PPARgammal, where the disorder is cancer, e.g. follicular carcinoma. The PAX8-PPARgammal molecules are also useful for providing nucleotide and amino acid sequences useful for detecting the above disease. The present sequence represents a human PAX867-PPARgammael polypeptide
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                                                                                                                                                                                                                                                        PAX8-PPARgammal; oncogene; cytostatic; PAX8; PPARgammal; cancer; follicular carcinoma; PAX8e7-PPARgammael; human; ss.
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Pred. No. 0.017;
0; Mismatches 1;
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                                                                                                                                                                                            Human PAX8e7-PPARgammae1 cDNA sequence.
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1..2334
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AAH76281 standard; cDNA; 2334 BP.
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ilarity 96.9%;
Conservative
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14-AUG-2000; 2000US-0225079
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Best Local Similarity
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                                                                                                                                         1169 CCATCGCAGGCATGGTGGCAGAAATGACCATGGTTGACACAG 1210
                                                                                              CCATCGCAGGCATGGTGGCAGAAATGACCATGGTTGACACAG 42
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   100.0%; Pred. No. 3.4e-07;
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                              0; Mismatches
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3..41
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14-AUG-2000; 2000US-0225079.
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Best Local Similarity 100.
Matches 42; Conservative
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MPI; 2001-514487/56.

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26-JUL-2001

lomo sapiens

29-OCT-2001

AAH76284;

AAH76284 ID AAH7

Op

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P-PSDB; AAB85796

Local Similarity

Query Match

31;

11 Matches

11

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RESULT 5 AAH76281

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Gaps

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Indels

22; Length 2334;

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us-09-765-111a-11.rng

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The invention relates to a novel method for diagnosing and detecting the progression of liver cancer, hepatocellular carcinoma or metastatic liver tumour in a patient, and differentiating metastatic liver cancer from hepatocellular carcinoma in a patient, involving detecting the level of expression of two or more genes represented in ABN93503-ABN97455 in a tissue sample. The method of the invention has hepatocropic, and cytostatic activity. The method is useful for diagnosing and detecting the progression of liver cancer, hepatocellular carcinoma and metastatic
                                                                                                                                                              The invention relates to an oncogene designated PAX8-PPARgammal that contains a PAX8 coding region fused to PPARgammal coding region. The PAX8-PPARgammal polypeptides can be expressed by standard recombinant methodology, A PPARgammal ligand or agent is useful for treating a subject having a disorder characterized by the presence of a PAX8-PPARgammal, where the disorder is cancer, e.g. follicular carcinoma. The PAX8-PPARgammal molecules are also useful for providing nucleotide and amino acid sequences useful for detecting the above disease. The present sequence represents a human PPARgamma polypeptide encoding cDNA.
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                                             New PAX8-PPARc1 oncogene and oncoprotein, useful for detecting and treating certain tumors or cancers, e.g. follicular carcinoma
                                                                                                                                                                                                                                                                                                                                                                                                                                                     71.4%; Score 30; DB 22; Length 1811;
86.8%; Pred. No. 0.023;
vative 0; Mismatches 5; Indels 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gene #2212 used to diagnose liver cancer.
                                                                                                                        Disclosure; Page 137-139; 145pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Peres-Da-Silva S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 1; SEQ ID NO 2212; 298pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ABN95714 standard; DNA; 1811 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           02-OCT-2000; 2000US-237054P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              02-OCT-2001; 2001WO-US30589
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    13-AUG-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches 33; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (GENE-) GENE LOGIC INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Horne D, Alvares C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2002-426119/45.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                liver tissue sample
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
     P-PSDB; AAB85802.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO200229103-A2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ABN95714;
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ABN95714
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           receptor-gammal (PPAR-gammal).
The invention relates to a method for identifying nuclear receptor agonists and antagonists comprises measuring fluorescent resonance energy transfer between fluorescent-labelled nuclear receptors and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           for identifying agonists and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    the human peroxisome proliferator activated
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            71.4%; Score 30; DB 20; Length 1811; 86.8%; Pred; No. 0.023;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 1811 BP; 510 A; 433 C; 422 G; 446 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                          Identifying nuclear receptor agonists and antagonists
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Zhou G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CGCAGGCATGGTGGCAGAAATGACCATGGTTGACACAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           co-activators. The method can be used antagonist of nuclear receptors.
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                                                                                                                                                                                                                                                                                      Moller DE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
173..1609
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; Fig 9b; 60pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAH76296 standard; cDNA; 1811
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human PPARgamma cDNA sequence.
                                                                                                                                          98WO-US21049.
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14-AUG-2000; 2000US-0225079.
                                                                                                                                                                                       97US-0061385
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                                                                                                                                                                                                                                                                                    Cummings RT, Hermes JD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Kroll TG, Fletcher JA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /*tag=
                                                                                                                                                                                                                                         (MERI ) MERCK & CO INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This sequence encodes
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P-PSDB; AAY05471.
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nes 33; Conserv
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                                                                                                                                                                                         07-OCT-1997;
  Homo sapiens
                                                                                                                                          06-OCT-1998;
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                                               WO9918124-A1
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Matches
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                          expression profiles which serve as useful diagnostic markers as well as markers that can be used to monitor disease states, disease progression, drug toxicity, drug efficacy and drug metabolism.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present sequence encodes a human peroxisome proliferator-activated receptor gamma (PPAR-gamma) polypeptide. PPAR are orphan receptors, and may play a role in proliferative and differentiation aspects of cancer. The PPAR-gamma polynucloide is useful for detecting a mRNA transcript that encodes PPAR polypeptide. It is also useful for detecting hybrid formation. The PPAR-gamma polypeptide is useful in diagnostics, drug
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /product= "peroxisome proliferator-activated receptor
                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     proliferator-activated receptor gamma; PPAR-gamma;
liver carcinoma in a patient. The method is useful for identifying
                                                                                                                                                                                                                                                                                                                                                                                   .,
                                                                                                                                                                                                                                                                                                                     DB 24; Length 1811;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human peroxisome proliferator-activated receptor gamma DNA
                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                      Sequence 1811 BP; 510 A; 433 C; 422 G; 446 T; 0 other;
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                                                                                                                                                                                                                                                                                                                                                                                   s,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   154 CGCCGCCGTGGCCGCAGAATGACCATGGTTGACACAG 191
                                                                                                                                                                                                                                                                                                                                                                                                                                              5 CGCAGGCATGGTGGCAGAATGACCATGGTTGACACAG 42
                                                                                                                                                                                                                                                                                                                     Score 30; DB 24;
Pred. No. 0.023;
                                                                                                                                                                                                                                                                                                                                                                                   0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAF55663 standard; DNA; 1844 BP.
                                                                                                                                                                                                                                                                                                                 71.4%;
86.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                   33; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (ARCH-) ARCH DEV CORP.
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                                                                                                                                                                                                                                                                                                                                                      Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            receptor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 08-OCT-1993;
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DB 22; Length 1844; 0.023;

Score 30; Pred. No.

71.4%; 86.8%;

Query Match Best Local Similarity

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Mammal, human, rhesus monkey, baker's yeast, fission yeast, Norway rat, mouse; Chinese hamster, African clawed frog; fruit fly, dog; leukaemia; cancer, Tymphoma, neuroblastcoma; autoimmune disorder, cell proliferation, nervous system disorder; inflammatory disorder; cell differentiation, despensit, stem cell growth factor; activin; inhibin; cartilage; burn; genetic disorder; born ergeneration; tendon; ligament; tissue repair; cytostatic; antirheumatic; antiattic; vulnerary; antiinflammatory; antibacterial; immunosuppressive, vasotropic, antipathmatic; antiallergic; neuropictective; osteopathic; antidiabetic; antipathmatic; antiallergic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           contig polynucleotides encoding polypeptides of the invention. The DNA and protein sequences are useful for the treatment, diagnosis and prevention of various types of disorder in a mammalian subject such as a human, dog, monkey, mouse, hamster or rat. The disorders include cancers such as leukaemia, lymphoma and neuroblastoma, autoimmune disorders such as multiple sclerosis, connective tissue disease, rheumatoid arthritis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               diabetes mellitus, allegic rhinitis, asthma and eczema, nervous system disorders such as Parkinson's disease, Alzheimer's disease, Huntington's chorea, amyotrophic lateral solerosis, spinal muscular atrophy and wernicke disease, inflammatory disorders such as nephritis, Crohn's disease, ischaemia-reperfusion injury, shock, sepsis and inflammatory bowel disease. The sequences exhibit activity relating to angiogenesis, ell proliferation, cell differentiation, stem cell growth factor, activity relating to inhibit factor, activity can be used to manipulate stem cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ren F;
Xu C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Novel polypeptides and nucleic acids obtained from cDNA libraries prepared from various human tissues, for diagnosis, treatment of cancer, neurological, inflammatory disorders and for use in arrays for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequences AAS44576-AAS44919 represent full-length polynucleotides and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Zhang J, Zhao QA, Re
Ma Y, Wang D, Chen
                                     154 ceccecerececedadaneaccarecreacacae 191
5 CGCAGGCATGGTGGCAGAATGACCATGGTTGACACAG 42
                                                                                                                                                                                                                                                                  Human full-length polynucleotide sequence #78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           immunostimulant; analgesic; gene therapy.
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F, Wang J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 1; SEQ ID No 78; 153pp; English.
                                                                                                                                               BP.
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Wehrman T,
                                                                                                                                             AAS44653 standard; DNA; 2295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           28-FEB-2000; 2000US-0515126.
18-MAY-2000; 2000US-0577409.
17-JUN-2000; 2000US-0597707.
14-JUL-2000; 2000US-0516807.
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                                                                                                                                                                                                                        18-DEC-2001 (first entry)
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Xue AJ, Yang Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          P-PSDB; AAU27753
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                                                                                                     RESULT 10
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Best Local Similarity
Matches 28; Conserv
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in culture to give rise to neuroepithelial cells that can be used to augment or replace cells damaged by illness, accidental damage or genetic disorders. The sequences may also be used for regeneration of bone, cartilage, tendons and ligaments and in tissue repair and burn healing. Note: Some sequences for this patent did not form part of the printed specification, but were obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention relates to an oncogene designated PAX8-PPARgammal that contains a PAX8 coding region fused to PPARgammal coding region. The PAX8-PPARgammal polypeptides can be expressed by standard recombinant methodology. A PPARgamma ligand or agent is useful for treating a subject having a disorder characterized by the presence of a PAX8-PPARgammal, where the disorder is cancer, e.g. follicular carcinoma. The PAX8-PPARgammal molecules are also useful for providing nucleotide and amino acid sequences useful for detecting the above disease. The present sequence represents the nucleotide sequence including and surrounding the fusion juncture in the PAX8e8-PPARgammael DNA.
                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New PAX8-PPARCI oncogene and oncoprotein, useful for detecting and treating certain tumors or cancers, e.g. follicular carcinoma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PAX8; PPARgammal; cancer;
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                                                                                                                                                                                      71.4%; Score 30; DB 22; Length 2295; 86.8%; Pred, No. 0.025; ive 0; Mismatches 5; Indels (
                                                                                                                                                        Sequence 2295 BP; 525 A; 606 C; 565 G; 599 T; 0 other;
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follicular carcinoma; PAX8e8-PPARgammael; human; ss.
                                                                                                                                                                                                                                                                                                 1658 CGCCGCCGTGGCCGCAGAATGACCATGGTTGACACAG 1621
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PAX8e8-PPARgammael fusion juncture DNA sequence.
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                                                                                                                                                                                                                                                                       5 CGCAGGCATGGTGGCAGAAATGACCATGGTTGACACAG 42
                                                                                                               at ftp.wipo.int/pub/published_pct_sequences.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 21; Page 118; 145pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                          ВР
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14-AUG-2000; 2000US-0225079.
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Matches 33; Conserv
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AAH76285
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Length 42;

58.1%; Score 24.4; DB 22;

Query Match

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                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention relates to an oncogene designated PAX8-PPARgammal that
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PAX8-PPARgammal; oncogene; cytostatic; PAX8; PPARgammal; cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        useful for detecting follicular carcinoma
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                             Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      follicular carcinoma; PAX8e8-PPARgammae1; human; ss.
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82.4%; Pred. No. 1.8;
tive 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New PAX8-PPARc1 oncogene and oncoprotein,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                treating certain tumors or cancers, e.g.
                                                                                                                                                                                                                                                                                                                                                                                                                 Human PAX8e8-PPARgammae1 cDNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 1; Page 106-109; 145pp; English.
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ID AAD21022 standard; cDNA; 1518 BP.
                                                                                                                                                                                                                                                           ВР.
                                                                                                                                                                                                                                                        AAH76282 standard; cDNA; 2523
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14-AUG-2000; 2000US-0225079.
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                             Conservative
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follicular carcinoma; PPARgamma; human; ss.
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                       Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                           peroxisome proliferator activated receptors (PPAR) gammal and gammal.

The invention is useful for treating cancer and other disorders including excessive cell proliferation and viral infection. The invention is also directed to the use of PPAR gammal and gammal to identify compounds that are antiproliferative, antiviral and antitumour agents. The invention also relates to a method of treating cancer using a pharmaceutical composition comprising this accordance using a pharmaceutical composition comprising this accoldance in an amount sufficient to modulate PPAR gammal and gammal activity. The present cDNA sequence encodes human peroxisome proliferator activated receptor (PPAR) gammal
                                                                       Human, peroxisome proliferator activated receptor gamma2, PPAR gamma2, cytotoxic, antiproliferative, antiviral, cancer, cell proliferation, viral infection; pharmaceutical; thiazolidinedione; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                   Human peroxisome proliferator activated receptor (PPAR) gamma2 cDNA.
                                                                                                                                                                       /product= "Human peroxisome proliferator activated receptor (PPAR) gamma2 protein"
                                                                                                                                                                                                                                                                                                                                                                           Use of thiazolidinedione for treating cancer and viral infections
                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to compounds and ligands that bind to human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PAX8-PPARgammal; oncogene; cytostatic; PAX8; PPARgammal; cancer;
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8
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Pred. No. 5;
0; Mismatches
                                                                                                                                      Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              protein related to the invention
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97US-0844007.
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29; Conservative
                              (first entry)
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/*tag=
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P-PSDB; AAE12868.
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Best Local Similarity
Matches 29; Conserv
                                                                                                                   Homo sapiens.
                                                                                                                                                                                                                                                                   02-MAY-1996;
18-APR-1997;
                                                                                                                                                                                                     US6294559-B1
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                              15-JAN-2002
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           AAD21022;
                                                                                                                                                                                                                                                                                                                      Smith RG;
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                                                                                                                                       Key
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Contains a PAX8 coding region fused to PPARgammal coding region. The PAX8-PPARgammal polypeptides can be expressed by standard recombinant methodology. A PPARgamma ligand or agent is useful for treating a subject having a disorder characterized by the presence of a PAX8-PPARgammal, where the disorder is cancer, e.g. follicular carcinoma. The PAX8-PPARgammal molecules are also useful for providing nucleotide and amino acid sequences useful for detecting the above disease. The present sequence represents a human PPARgamma polypeptide encoding cDNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Cytostatic; antiinflammatory, antisense oligonucleotide; PPARgamma; peroxisome proliferator-activated receptor gamma; transcription factor; nuclear hormone receptor; human; infection; inflammation; tumour; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention relates to an oncogene designated PAX8-PPARgammal that
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New PAX8-PPARc1 oncogene and oncoprotein, useful for detecting and treating certain tumors or cancers, e.g. follicular carcinoma
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 57.6%; Score 24.2; Di
Best Local Similarity 78.4%; Pred. No. 5.1;
Matches 29; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure; Page 123-125; 145pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (BGHM ) BRIGHAM & WOMENS HOSPITAL INC.
Location/Qualifiers
91..1608
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                                                                                                                                                                                                                                                                                                     18-JAN-2001; 2001WO-US01664.
                                                                                                                                                                                                                                                                                                                                                                                20-JAN-2000; 2000US-0177109.
14-AUG-2000; 2000US-0225079.
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                                                                           /*tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2001-514487/56.
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(ISIS-) ISIS PHARM INC.

Borchers AH; McKay R, Baker BF,

WPI; 2001-070112/08. P-PSDB; AAB59839.

Novel antisense compounds capable of modulating expression of peroxisome proliferator-activated receptor gamma useful for diagnosis, prophylaxis and treatment of diseases associated with expression of the receptor

Example 13; Column 45-48; 40pp; English.

Peroxisome proliferator-activated receptors (PPARs) are members of the nuclear hormone receptor subfamily of transcription factors. The present invention relates to antisense oligonucleotides (see AAF23652-F23711), targeted to a nucleic acid molecule encoding human PPARgamma, which sepecifically hybridises with and inhibits the expression of human PPARgamma. The present sequence is the coding sequence for human PPARgamma. The PPARgamma antisense oligonucleotides of the present invention can be used in the diagnosis and treatment of diseases associated with the expression of PPARgamma, e.g. to prevent or delay infection, inflammation or tumour formation. 

Sequence 1608 BP; 462 A; 380 C; 361 G; 405 T; 0 other;

Gaps ; Query Match
57.6%; Score 24.2; DB 22; Length 1608;
Best Local Similarity 78.4%; Pred. No. 5.1;
Matches 29; Conservative 0; Mismatches 8; Indels 0;

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6 GCAGGCATGGTGGCAGAATGACCATGGTTGACACAG 42 ò

157 GCAAACATATCACAAGAAATGACCATGGTTGACACAG 193

Search completed: January 21, 2003, 23:09:56 Job time : 129.667 secs

us-09-765-111a-11.rni

Sequence 2 Sequence 1 Sequence 1 Sequence 1 Sequence 1 Sequence 1

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US-08-484-200-1
US-08-477-493-1
US-09-465-375-1
US-09-788-070-1
US-09-26-059-29
US-08-651-472-18
US-08-651-472-18
US-08-131-995-12
US-08-131-995-12
US-08-131-995-12
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NAME: Katz, Martin L.
REGISTRATION NUMBER: 25,011
REFERENCE/DOCKET NUMBER: ARCH:098
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-616-5400
TELEFAX: 312-616-5400
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
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STREET: 2 ...
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                                                                                                                                                          January 21, 2003, 23:03:25; Search time 26:3333 Seconds (without alignments) 489.130 Million cell updates/sec
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Copyright (c) 1993 - 2003 Compugen Ltd.
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US-09-128-142-3
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US-08-917-653-3
US-08-917-65-3
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No.
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Sequence 12, Appl
Patent No. 5200340
Sequence 1, Appli
Sequence 5, Appli
Sequence 7, Appli
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                                                                                                                                                                                                                                                                  Sequence 1, Application US/08134557D
Patent No. 6200802
GENERAL INVENTATION:
APPLICANT: Blumberg, Bruce
TITLE OF INVENTION: Human Peroxisome Proliferator Activated
TITLE OF SEQUENCES: 8
CORRESPOND::CE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: Rockey, Milnamow & Katz, Ltd.
STREET: 2 Prudential Plaza, Suite 4700 180 N. Stetson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: BATENIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/134,557D
FILING DATE:
CLASSIFICATION: 435
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GENERAL INFORMATION:
APPLICANT: TANABE SETYAKU CO. LID.
APPLICANT: TANABE SETYAKU CO. LID.
APPLICANT: TANABE SETYAKU CO. LID.
APPLICANT: TANGURAH, JUUKO
TITLE OF INVENTION: METHOD FOR IDENTIFYING OR SCREENING AGONIST AND ANTAGONIST TO PF
FILE REPERENCE: TANGURAH:
CURRENT APPLICATION NUMBER: U$/09/514,247A
CURRENT FILING DATE: 2000-02-28
                                                                                                                                                                                                                          0;
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) Sequence 4, Application US/08917653
) Patent No. 6004751
) GENERAL INFORMATION:
APPLICANT: Rosenfield, Robert L.
ITILE OF INVENTION: IDENTIFICATION OF ACTIVATORS AND TITLE OF INVENTION: INHIBITORS OF SEGUM FORMATION
CORRESPONDENCE 3.
CORRESPONDENCE ADDRESS:
ADDRESSES: Arnold, White & Durkee
STREET: P.O. Box 4433
                                                                                                                                                                                                                        Indels
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COMPUTER READABLE FORM:
MEDIUW TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
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                                                                                                                                                                        57.6%; Score 24.2; DB 3; 78.4%; Pred. No. 1.3; tive 0; Mismatches 8;
                                                                                                                                                                                                                                                                                                         157 GCAAACATATCACAAGAAATGACCATGGTTGACACAG 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              225 GCAAACATATCACAAAATGACCATGGTTGACACAG 261
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION NUMBER: PCT/JP98/03734
PRIOR FILING DATE: 1998-08-24
PRIOR APPLICATION NUMBER: JP231084/1997
PRIOR FILING DATE: 1997-08-27
NUMBER OF SEQ ID NOS: 10
SOFTWARE: Patentin version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                        ; Sequence 5, Application US/09514247A; Patent No. 6365361
                                                                                                                                                              Query Match 57.0%
Best Local Similarity 78,4%
Matches 29; Conservative
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Best Local Similarity 78.4
Matches 29; Conservative
                                                                                                  LOCATION: (91) ... (1608)
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                            ORGANISM: Homo sapiens
FEATURE:
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ORGANISM: Homo sapiens
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STATE: Texas
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                                                                               NAME/KEY: CDS
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US-09-514-247A-5
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                                                                                                                                                                                           AL INFORMALION.
APPLICANT: SMITH, ROY G.
TITLE OF INVENTION: ANTI-PROLIFERATIVE AGENTS ASSOCIATED WITH
TITLE OF INVENTION: PEROXISOME PROLIFERATOR ACTIVATED RECEPTORS GAMMAI AND GAMM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: ROBERT MCKAY
APPLICANT: Alexander H. Borchers
APPLICANT: Alexander H. Borchers
APPLICANT: Alexander H. Borchers
APPLICANT: Alexander H. Borchers
APPLICANT: Alexander H. Borchers
APPLICANT: Alexander H. Borchers
TITLE OF INVENTION: ANTISENSE MODULATION OF PEROXISOME PROLIFERATOR-ACTIVATED RECEPTO
FILE REFERENCE: RTS-0104
CURRENT APPLICANTION NUMBER: US/09/484,345
NUMBER OF SEQ ID NOS: 90
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MEDIUM TYPE: Rloppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: Power Macintosh 7500/100
SOFTWARE: Microsoft Word 6.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/128,142
FILING DATE: 03-Aug-1998
CLASSIFICATION: CHNKNOWN>
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
ADDRESSEE: Jack L. Tribble
STREET: 126 E. Lincoln Ave., P.O. Box 2000
154 CGCCGCCGTGGCCGCAGAATGACCATGGTTGACACAG 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       67 GCAAACATATCACAAGAAATGACCATGGTTGACACAG 103
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REGISTRATION NUMBER: 32,633
REPERDENCE/POCKET NUMBER: <UNKNOWN-
TELECOMMUNICATION INFORMATION:
TELEPHONE: (908) 594-5321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: 08/844,007
FILING DATE: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 1518 base pairs
TYPE: nucleic acid
STRANDEDMESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
SEQUENCE DESCRIPTION: SEQ ID NO: 3:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 3, Application US/09484345
Patent No. 6159734
GENERAL INFORMATION:
                                                                                                                                        Sequence 3, Application US/09128142 Patent No. 6294559 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Tribble, Jack L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
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INFORMATION FOR SEQ ID NO: 3:
                                                                                                                                                                                                                                                                                                                                                                                                STATE: New Jersey
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                                                                                                                                                                                                                                                                                                                                                                             CITY: Rahway
                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY: US
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Best Local Similarity
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LENGTH: 1608
                                                                                                                     US-09-128-142-3
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US-09-589-927-3/c

Sequence 3, Application US/0958927

Sequence 3, Application US/0958927

Sequence 3, Application US/0958927

Sequence 3, Application US/0958927

GENERAL INFORMATION:

TITLE OF INVENTION: Modify Cell and Tissue Interactions

TITLE OF INVENTION: Modify Cell and Tissue Interactions

FILE REPERRINCE: 942521

CURRENT APPLICATION NUMBER: US/09/589,927

NUMBER OF SEQ ID NOS: 12

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 3, Application US/09277665

Patent No. 6447729

CENERAL INCORMATION:
APPLICANT: University of Kansas Medical Center
TITLE OF INVENTION: The Use of Isolated Domains of Type IV Collagen to
TITLE OF INVENTION: Modify Cell and Tissue Interactions
FILE REPRENCE: 94525-1
CURRENT APPLICATION NUMBER: US/09/277,665
NUMBER OF SEQ ID NOS: 12
SOFTWARE: Patentin Ver. 2.0
SSEQ ID NO 3
LENGTH: 900
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80.6%; Pred. No. 15;
tive 0; Mismatches
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Patent No. 64261B
; GENERAL INFORMATION:
APPLICANT: Jones, Karen A.
; APPLICANT: Volkmuth, Wayne
120 AGAAATTACCATGGTTGACACAG 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 80.6%
Matches 25; Conservative
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Best Local Similarity 80.61
Matches 25; Conservative
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; LOCATION: (40)..(813)
US-09-277-665-3
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US-09-589-927-3
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ORGANISM: Human
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-484-970B-4/C
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                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH:
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                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 21.4; DB 3; Length 277; Pred. No. 12; 0; Mismatches 1; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 51.0%; Score 21.4; DB 3; Length 373; Best Local Similarity 95.7%; Pred. No. 12; Matches 22; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: ROSenfield, Robert L.
TITLE OF INVENTION: IDENTIFICATION OF ACTIVATORS AND
NUMBER OF SEGURNESS: 4
CORRESPONDENCE ADDRESS: 4
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IN PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PREPRINT Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION DATA:
CLASSIFICATION TOWBER: US/08/917,653
FILING DATE: Concurrently Herewith
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Highlander, Steven L.
REGISTRATION NUMBER: 37,642
REGISTRATION NUMBER: 37,642
REGISTRATION NUMBER: ARCD:216
TELECOMMUNICATION INPORMATION:
TELECOMMUNICATION INPORMATION:
TELEPHONE: (512) 418-3000
                                                                                   ATTORNEY/AGENT INFORMATION:
NAME: Highlander, Steven L.
REGISTRATION NUMBER: 37,642
REFERENCE/DOCKET NUMBER: ARCD:216
TELECOMMUNICATION INFORMATION:
TELEPHONE: (512) 418-3000
TELEPAX: (512) 414-7577
INPORMATION FOR SEQ ID NO: 4: SEQUENCE CHARACTERISTICS:
LENGTH: 277 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                          APPLICATION NUMBER: US/08/917,653
FILING DATE: Concurrently Herewith
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           82 AGAAATTACCATGGTTGACACAG 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 3, Application US/08917653
Patent No. 6004751
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEPAX: (512) 474-7577
INFORMATION FOR SEQ ID NO: 3: SEQUENCE CHARACTER.ESTICS: LENGTH: 373 base pairs TYPE: nucleic acid STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                         51.0%;
95.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity 95.7 es 22; Conservative
    CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ZIP: 77210
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy of
                                                                                                                                                                                                                                                                                                                                                                      linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CITY: Houston
STATE: Texas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     U.S.
                                                                                                                                                                                                                                                                                                                                                                      ; TOPOLOGY:
US-08-917-653-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 6
US-08-917-653-3
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Onery Match

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Gaps 0 Ö

Gaps

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20 AGAAATGACCATGGTTGACACAG 42

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1 CCATCGCAGGCATGGTGGCAGAATGACCATGGTTGACACAG 42
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US-08-735-609-4
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                                                                                                                                                                                                                                                                                                                                                                         51.0%; Score 21.4; DB 4; Length 4359; 80.6%; Pred. No. 19; cive 0; Mismatches 6; Indels 0
                                                                                                                                                                                                                                                                                 NAME/KEY: misc_feature
OTHER INFORMATION: Incyte ID No. 6426186 331365 (1553795CB1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
SOFTWARE: Patentin Release #1.0, Version #1.30
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/735,609
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Ingolia, Dane E.
REGISTRATION UNMEER: UM-02484
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 705-8410
TELEFAX: (415) 397-8838
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARRACTERISTICS:
LENGTH: 34303 base pairs
TYPE: nucleic acid
TYPE: nucleic acid
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
APPLICANT: Chamberlain, Jeffrey S.
APPLICANT: Amalfitano, Andrea
APPLICANT: Hauser, Michael A.
APPLICANT: Kumz-Singh, Rajendra
APPLICANT: Hartigan-O'Connor, Dennis J.
TITLE OF INVENTION: IMPROVED ADENOVIRUS VECTORS
NUMBER OF SEQUENCES: 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STREET: 220 Montgomery Street, Suite 2200 CITY: San Francisco STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3054 Geregearagradadacarcaccaggerra 3024
APPLICANT: Walker, Michael G.
TITLE OF INVENTION: BONG REMODELING GENES
FILE REFRENCE: P8-0014 US
CURRENT APPLICATION NUMBER: US/09/484,970B
CURRENT FILING DATE: 2000-01-18
NUMBER OF EQ ID NOS:
SOFTWARE: PERL PROGram
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      6 GCAGGCATGGTGGCAGAAATGACCATGGTTG 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             United States Of America
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "DNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Seguence 4, Application US/08735609
Patent No. 5955360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ouery Match
Best Local Similarity 69.0°
Matches 29; Conservative
                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 80.65
Matches 25; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ZIP: 94104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
ADDRESSEE: Medlen &
                                                                                                                                                                                                               TYPE: DNA ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRANDEDNESS:
TOPOLOGY: lin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              94104
                                                                                                                                                                                         LENGTH: 4359
                                                                                                                                                                                                                                                                                                                                US-09-484-970B-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-08-735-609-4
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Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
COMPUTER: FEM PC COMPACE: PC-DCS
COFERATING SYSTEM: PC-DCS/MS-DCS
SOFTWARE: PatentIn Release #1.0, Version #1.30
Db 18736 CCACAGAGGCATGGAGACACAAACGTCCCCGGTTGCCTCAG 18777
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        pb 18736 ccacadadddarddadacacaaaccroccogrigocroad 18777
                                                                                                                                                                                                                                     APPLICANT: Chamberlain, Jeffrey S.
Amalfitano, Andrea
Hauser, Michael A.
Kumara-Singh, Rajendra
Harrigan-O'Connor, Dennis J.
TITLE OF INVENTION: IMPROVED ADENOVIRUS VECTORS
                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
AMORIAN CARTOLL LLP
STREET: 220 Montgomery Street, Suite 2200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 CCATCGCAGGCATGGTGGCAGAAATGACCATGGTTGACACAG 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Hauser, Michael A.
APPLICANT: Kumar-Singh, Rajendra
APPLICANT: Hartigan-O'Connor, Dennis J.
TITLE OF INVENTION: IMPROVED ADENOVIRUS VECTORS
NUMBER OF SEQUENCES: 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFE SUCE/DOCKET NUMBER: UM-02484 TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CITY: San Francisco
STATE: California
COUVRRY: United States Of America
ZIP: 94104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US/08/735,609
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DESCRIPTION: /desc = "DNA"
SEQUENCE DESCRIPTION: SEQ ID NO: 4:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Ingolia, Diane E. REGISTRATION NUMBER: 40,027
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Chamberlain, Jeffrey S. APPLICANT: Amalfitano, Andrea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEPHONE: (415) 705-8410
TELEFAX: (415) 397-8338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE: 23-Oct-1996
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 34303 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 4, Application US/09315372; Patent No. 6057158; GENERAL INFORMATION:
                                                                                                                                                   Sequence 4, Application US/08735609; Patent No. 5994132; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION DATA:
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DB 3; Length 34303;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Mismatches 13; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Db 18736 ccacadagggcarggagacacaaaaccrccccccrrac 18777
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ZIP: 94104
COMPUTER READABLE FORM:
COMPUTER: READABLE FORM:
COMPUTER: ISM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTMARE: PARENTIN RELEASE #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/245,497
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Hauser, Michael A.
APPLICANT: Kumar-Singh, Rajendra
APPLICANT: Hartigan-O'Connor, Dennis J.
TITLE OF INVENTION: IMPROVED ADENOVIRUS VECTORS
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 CCATCGCAGGCATGGTGGCAGAAATGACCATGGTTGACACAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: Medlen & Carroll, LLP
STREBT: 220 Montgomery Street, Suite 2200
STREB: San Francisco
STATE: California
COUNTRY: United States Of America
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  50.5%; Score 21.2; 1 69.0%; Pred. No. 34;
                                                                                           NAME: Ingolia, Diane E.
REGISTRATION NUMBER: 40.027
REFERENCE/DOCKET NUMBER: UM-02484
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 705-8410
TELEFAX: (415) 397-8338
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 34303 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/735,609
APPLICATION NUMBER: 68) FILING DATE:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    UM-02484
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Sequence 4, Application US/09245497

Patent No. 6083750

GENERAL INFORMATION:

APPLICANT: Chamberlain, Jeffrey S.

APPLICANT: Amalfitano, Andrea
                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: other nucleic acid DESCRIPTION: /desc = "DNA"
                      APPLICATION NUMBER: 08/735,609
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: INGOLIA, Diane E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: INGOLIA, DIANE E.
REGISTRATION NUMBER: 40,027
REFERENCE/DOCKET NUMBER: UM-07
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 375-8410
TELEFFX: (415) 376-8410
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 34303 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ouery Match
Best Local Similarity 69.08
Matches 29; Conservative
                                                                                                                                                                                                                                                                                                                TYPE: nucleic acid
STRANDEDNESS: double
  PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                  linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE
                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-244-752-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 21.2; DB 3; Length 34303; Pred. No. 34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    50.5%; Score All. , 69.0%; Pred. No. 34; of Mismatches 13; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Db 18736 CCACAGAGGCATGGAGACACAAACGTCCCCGGTTGCCTCAG 18777
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Chamberlain, Jeffrey S.
APPLICANT: Chamberlain, Jeffrey S.
APPLICANT: Amalfitano, Andrea
APPLICANT: Manifitano, Andrea
APPLICANT: Manifitano, Andrea
APPLICANT: Mars-Singh, Rajendra
APPLICANT: Hartigan-O'Connor, Dennis J.
TITLE OF INVENTION: IMPROVED ADENOVIRUS VECTORS
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSES Medien & Carroll, LLP
STREET: 220 Montgomery Street, Suite 2200
CITY: San Francisco
STATE: California
COUNTEX: United States Of America
ZIP: 94104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 CCATCGCAGGCATGGTGGCAGAAATGACCATGGTTGACACAG 42
                                                                                                                                                                                                                                                       SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/315,372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/244,752 CLASSIFICATION:
                   ADDRESSEE: Medlen & Carroll, LLP STREET: 220 Montgomery Street, Suite 2200
                                                                                                                    United States Of America
                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/735,609
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         UM-02484
                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: other nucleic acid DESCRIPTION: /desc = "DNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE INGUIA, DIANE E.
REGISTRATION NUMBER: 40,027
REFERENCE/DOCKET NUMBER: UM-07
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 705-8410
TELEFAX: (415) 37-8338
INFORMATION FOR SEO ID NO: 4:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; Sequence 4, Application US/09244752 tent No. 6063622
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 34303 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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Best Local Similarity 69.0%
Matches 29; Conservative
CORRESPONDENCE ADDRESS:
                                                                     San Francisco
                                                                                           California
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                                                                                                                  COUNTRY: Un
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US-09-244-752-4
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                                                                                                     DB 3; Length 34303;
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                                                                                                   Query Match 50.5%; Score 21.2; DB 3; Length 3 Best Local Similarity 69.0%; Pred. No. 34; Matches 29; Conservative 0; Mismatches 13; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION UNBER: US/09/562,919
FLING DATE: 02-May-2000
CLASSIFICATION: <UNKnown>
                                                                                                                                                                                                                                                                                                                                                                Sequence 4. Application US/09562919

Patent No. 645156

GENERAL INFORMATION:

APPLICANT: Chamberlain, Jeffrey S.

Amalfitano, Andrea

HAUSEN: Michael A.

Kumar-Singh, Rajendra

HATLE OF INVENTION: IMPROVED ADENOVIRUS VECTORS

NUMBER OF SEQUENCES:

CORRESPONDENCE ADDRESS:

ADDRESSE:

ADDRESSE:

Median & Carroll, LLP

STREET: 220 Montgomery Street, Suite 2200

CITY: San Francisco

STRATE: California

COUVINY: United States Of America

ZIP: 94104

COMPTER FRADABLE FORM:
                                                                                                                                                                                                                                                Db 18736 CCACAGAGGCATGGAGACACAAACGTCCCCGGTTGCCTCAG 18777
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PREDICATION NUMBER: US/08/735,609
FILING DATE: 23-Oct -1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER: UM-02484
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 705-8410
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            )

DESCRIPTION: /desc = "DNA"

SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-09-562-919-4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear MOLECULE TYPE: other nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Ingolia, Diane E. REGISTRATION NUMBER: 40,027
// MOLECULE TYPE: other nucleic acid
// DESCRIPTION: /desc = "DNA"
US-09-245-497-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELETAX: (415) 397-8338
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 34303 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
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Best Local Similarity 69.0%
Matches 29, Conservative
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US-09-562-919-4
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Sequence 7, Appli
Sequence 26, Appli
Sequence 212, Ap
Sequence 8, Appli
Sequence 9, Appli
Sequence 9, Appli
Sequence 15, Appli
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Sequence 22, Appl
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Sequence 24, Appl
Sequence 990, App
                                                                                                                                                           January 21, 2003, 23:59:20 ; Search time 27 Seconds (without alignments) 693.573 Million cell updates/sec
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Sequence 6261,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                1 ccatcgcaggcatggtggca.....aatgaccatggttgacacag 42
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1: /cgn2 6/ptodata/1/pubpna/USO7 PUBCOMB.seq:*
2: /cgn2 6/ptodata/1/pubpna/PCT NEW PUBLs.seq:*
3: /cgn2 6/ptodata/1/pubpna/USO6 NEW PUBLs.seq:*
4: /cgn2 6/ptodata/1/pubpna/USO6 NEW PUBLseq:*
5: /cgn2 6/ptodata/1/pubpna/USO6 NEW PUB.seq:*
6: /cgn2 6/ptodata/1/pubpna/USO8 NEW PUB.seq:*
7: /cgn2 6/ptodata/1/pubpna/USO8 NEW PUB.seq:*
9: /cgn2 6/ptodata/1/pubpna/USO8 NEW PUB.seq:*
9: /cgn2 6/ptodata/1/pubpna/USO8 NEW PUB.seq:*
10: /cgn2 6/ptodata/1/pubpna/USO9 NEW PUB.seq:*
11: /cgn2 6/ptodata/1/pubpna/USO9 PUBCOMB.seq:*
11: /cgn2 6/ptodata/1/pubpna/USO9 PUBCOMB.seq:*
11: /cgn2 6/ptodata/1/pubpna/USO0 PUBCOMB.seq:*
11: /cgn2 6/ptodata/1/pubpna/USO0 PUBCOMB.seq:*
13: /cgn2 6/ptodata/1/pubpna/USO0 PUBCOMB.seq:*
13: /cgn2 6/ptodata/1/pubpna/USO0 NEW PUB.seq:*
14: /cgn2 6/ptodata/1/pubpna/USO0 NEW PUB.seq:*
GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
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US-09-765-111A-5

US-09-765-111A-5

US-09-765-111A-1

US-09-765-111A-1

US-09-765-111A-26

US-09-816-828-9

US-09-816-828-9

US-09-816-828-9

US-09-86-111A-3

US-09-765-111A-15

US-09-765-111A-37

US-09-765-111A-37

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US-09-86-1

US-09-765-111A-37

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Maximum Match 100%
Listing first 45 summaries
                                                                                                       - nucleic search, using sw model
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Maximum DB seq length: 200000000
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20 22 52.4 343 9 US-09-878-178-990 Sequence 990, App 22 21.6 51.4 511 10 US-09-925-299-109 Sequence 109, App 22 21.6 51.4 51.0 2212 10 US-09-925-299-109 Sequence 109, App 22 21.6 51.4 51.0 2212 10 US-09-925-302-75 Sequence 75, App 22 21.2 50.5 32481 10 US-09-925-302-75 Sequence 75, App 22 21.2 50.5 35481 10 US-09-925-316-23 Sequence 2, App 12 21.2 50.5 35935 10 US-09-47-1018-23 Sequence 2, App 12 21.2 50.5 35935 10 US-09-725-378-4 Sequence 2, App 13 20.5 35935 10 US-09-725-378-4 Sequence 2, App 13 20.5 35935 10 US-09-725-378-4 Sequence 3, App 13 20.8 49.5 20.5 35935 10 US-09-725-378-5 Sequence 1, App 13 20.8 49.5 20.6 49.0 18-09-867-701-7320 Sequence 1, App 13 20.8 49.5 20.6 49.0 18-09-867-701-7320 Sequence 1, App 14 20.6 49.0 134 10 US-09-964-761-2092 Sequence 1, App 15 20.6 49.0 134 10 US-09-964-761-209 Sequence 1, App 15 20.6 49.0 134 10 US-09-964-761-209 Sequence 1, App 16 20.6 49.0 134 10 US-09-964-870-612 Sequence 1, App 17 10 US-09-964-870-612 Sequence 1, App 17 10 US-09-764-870-612 Sequence 1, App 17 10 US-09-764-870-612 Sequence 1, App 17 10 US-09-764-870-612 Sequence 1, App 18 20.6 49.0 32195 10 US-09-764-870-612 Sequence 1, App 18 20.6 49.0 32195 10 US-09-764-870-612 Sequence 1, App 18 20.6 49.0 32195 10 US-09-764-870-612 Sequence 1605, App 18 20.6 49.0 32195 10 US-09-764-870-612 Sequence 1605, App 18 20.6 49.0 32195 10 US-09-764-870-612 Sequence 1605, App 18 20.6 49.0 32195 10 US-09-764-870-612 Sequence 1605, App 18 20.6 49.0 32195 10 US-09-976-880-1605 Sequence 1605, App 18 20.6 49.0 32195 10 US-09-976-880-1605 Sequence 1605, App 18 20.6 49.0 32195 10 US-09-976-880-1605 Sequence 1605, App 18 20.6 49.0 32195 10 US-09-976-880-1605 Sequence 1605, App 18 20.6 49.0 32195 10 US-09-976-880-1605 Sequence 1605, App 18 20.6 49.0 32195 10 US-09-976-880-1605 Sequence 1605, App 18 20.6 49.0 32195 10 US-09-976-880-1605 Sequence 1605, App 18 20.6 49.0 32195 10 US-09-976-880-1605 Sequence 1605, App 18 20.6 49.0 32195 10 US-09-976-880-1605 Sequence 1605, App 18 20.6 49.0 32195 10 US-09-976-880-1605 Sequence 1605, A
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## CLGNMENT

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US-09-765-111A-11
US-09-765-111A-11
Partent No. US20020106796A1
Partent No. US20020106796A1
GENERAL INPOWATION:
APPLICANT: Fletcher, Jonathan A.
APPLICANT: Ktoll, Todd G.
TITLE OF INVENTION: AND POLYPEPTIDES AND USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CCATCGCAGGCATGGTGGCAGAAATGACCATGGTTGACACAG 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CCATCGCAGGCATGGTGGCAGAATGACCATGGTTGACACAG 42
                                                                                                                                                                  FILE REFERENCE: B0801/7196/FERPLESS AND USE;
FILE REFERENCE: B0801/7196/FERPLAT
CURRENT FILING DATE: 2001-01-18
FRIOR PELICATION NUMBER: US 60/177,109
FRIOR FILING DATE: 2000-01-20
FRIOR APPLICATION NUMBER: US 60/225,079
FRIOR APPLICATION NUMBER: US 60/225,079
NUMBER OF SEQ ID NOS: 47
SOFTWARE: FRSEEG FOR Windows Version 3.0
LENGTH: 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 22, Application US/09765111A; Patent No. US20020106796A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: DNA
ORGANISM: Homo Sapiens
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US-09-765-111A-11
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Matches
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Query Match 72.4%;
Best Local Similarity 96.9%;
Matches 31; Conservative
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Best Local Similarity 96.9
Matches 31; Conservative
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ORGANISM: Homo Sapiens
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; LOCATION: (1)...(2334)
US-09-765-111A-1
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LOCATION: (3)...(41)
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US-09-765-111A-26
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US-09-765-111A-1
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APPLICANT: Kroll, Todd G.
ITLE OF INVENTION: PAX8-PPARGamma NUCLEIC ACID MOLECULES
ITLE OF INVENTION: AND POLYBEPTIDES AND USES THEREOF
FILE REFERENCE: 80601/7196/ERP/MAT
CURRENT APPLICATION NUMBER: US/09/765,111A
CURRENT PILING DATE: 2001-01-18
PRIOR APPLICATION NUMBER: US 60/177,109
PRIOR FILING DATE: 2000-01-20
PRIOR FILING DATE: 2000-01-44
NUMBER OF SEQ ID NOS: 47
SOFTWARE: FASESEQ for Windows Version 3.0
LENGTH: 2596
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 5. Application US/09765111A

Patent No. US20020106796A1

GENERAL INDEMATION:
APPLICANN: Fletcher, Jonathan A.
APPLICANN: Froit, Todd G.
TITLE OF INVENTION: PAX8-PPARgamma NUCLEIC ACID MOLECULES
TITLE OF INVENTION: PAX8-PPARgamma NUCLEIC ACID MOLECULES
TITLE OF INVENTION: PAX8-PPARgamma NUCLEIC ACID MOLECULES
FILE REFERENCE: B0801/1196/ERP/MAT
CURRENT PELLING. AND POLYEPTIDES AND USES THEREOF
FILE REFERENCE: B0801/1196/ERP/MAT
CURRENT PELLING DATE: 2001-01-18

PRIOR FILING DATE: 2000-01-20

PRIOR FILING DATE: 2000-01-4

NUMBER OF SEQ ID NOS: 47

SOFTWARE: FastSEQ for Windows Version 3.0

SEQ ID NO 5

LENGTH: 2625
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; Patent No. US20020106796A1
; GENEAL INFORMATION:
APPLICANT: Fletcher, Jonathan A.
; APPLICANT: Kroll, Todd G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity 100.
Matches 42; Conservative
                                                                                                                                                                                                                                                                                                                                                                                             ) NAME/KEY: CDS
; LOCATION: (161)...(2596)
US-09-765-111A-22
                                                                                                                                                                                                                                                                                                                               TYPE: DNA ORGANISM: Homo Sapiens
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; LOCATION: (1)...(2625)
US-09-765-111A-5
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US-09-765-111A-5
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TITLE OF INVENTION: PAX8-PPARGamma NUCLEIC ACID MOLECULES
TITLE OF INVENTION: AND POLYPEPTIDES AND USES THEREOF
THE REPREBRICE: BO801/7196/ERP/MAT
CURRENT APPLICATION NUMER: US/09/765,111A
FRIGA REPLICATION NUMER: US/09/765,111A
FRIGA REPLICATION NUMBER: US 60/177,109
FRIGA REPLICATION NUMBER: US 60/225,079
FRICA RELING DATE: 2000-08-14
SOFTWARE: PASTESQ for Windows Version 3.0
SEQ ID NO 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 1, Application US/09765111A
Sequence 1, Application US/09765111A
Sequence 1, Application US/09765111A
SERVERLANT SECONOTO16796A1
APPLICANT: Fletcher, Jonathan A.
APPLICANT: Factor, Jonathan A.
TITLE OF INVENTION: PAX8-PRAGamma NUCLEIC ACID MOLECULES
TITLE OF INVENTION: PAX8-PRAGamma NUCLEIC ACID MOLECULES
TITLE OF INVENTION: AND POLYPEPTIDES AND USES THEREOF
CURRENT APPLICATION NUMBER: US/09/765,111A
CURRENT APPLICATION NUMBER: US 60/177,109
PRIOR APPLICATION NUMBER: US 60/177,109
PRIOR APPLICATION NUMBER: US 60/177,109
PRIOR APPLICATION NUMBER: US 60/225,079
PRIOR PRIOR APPLICATION NUMBER: US 60/225,079
NUMBER OF SEQ ID NOS: 47
SOFTWARE: FastSEQ for Windows Version 3.0
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; Patent No. US20020106796A1
; General INFORMATION:
; APPLICANT: Fletcher, Jonathan A.
; APPLICANT: Kroll, Todd G.
; TITLE OF INVENTION: PAX8-PPARgamma NUCLEIC ACID MOLECULES
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SEQ ID NO 8
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APPLICANT: Horne, Darci T.

APPLICANT: Wockley, Joseph G.

APPLICANT: Scherf, Uwe

APPLICANT: Gene Expression Profiles in Liver Cancer:

ITLE OF INVENTION: Gene Expression Profiles in Liver Cancer:

FILE REFREENCE: 44921-5020-W

CURRENT FILING DATE: 2001-06-14

PRIOR FILING DATE: 2000-06-14

PRIOR FILING DATE: 2000-06-14

PRIOR FILING DATE: 2000-06-14

PRIOR FILING DATE: 2000-06-14

PRIOR FILING DATE: 2000-10-02

NUMBER OF SEQ ID NOS: 3950

SOFTWARE: Patentin Ver: 2.1

SEQ ID NO 2212

'ENCHART: 1811
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US-09-880-107-2212
                                                                                                                                                                                                                                                                                                                                                                                                                              71.4%; Score 30; DB 10; Length 1811; 86.8%; Pred. No. 0.0089; Live 0; Mismatches 5; Indels (
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TITLE OF INVENTION: AND POLYPEPTIDES AND USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               154 CGCCGCCGTGGCCGCAGAAATGACCATGGTTGACACAG 191
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                  FILE REFERENCE: B0801/7196/ERP/MAT
CURRENT APPLICATION NUMBER: US/09/765,111A
CURRENT PILING DATE: 2001-01-18
PRIOR APPLICATION NUMBER: US 60/177,109
PRIOR FILING DATE: 2000-01-20
PRIOR FILING DATE: 2000-01-20
PRIOR FILING DATE: 2000-08-14
NUMBER OF SEQ ID NOS: 47
SOFTWARE: FRAISEQ for Windows Version 3.0
SEQ ID NO 26
LENGTH: 1811
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 2212, Application US/09880107 Patent No. US20020142981A1
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; Sequence 8, Application US/09816828
; Patent No. US20020150898A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INPORMATION:
APPLICANT: Tang, Y. Tom
APPLICANT: Zhou, Ping
APPLICANT: Acodition, Ryle
APPLICANT: Acundi, Vinod
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity 86.83 thes 33; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        33; Conservative
                                                                                                                                                                                                                                                                                                                                    ) NAME/KEY: CDS
; LOCATION: (173)...(1609)
US-09-765-111A-26
                                                                                                                                                                                                                                                                     TYPE: DNA
ORGANISM: Homo Sapiens
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ORGANISM: Homo sapiens
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Best Local Similarity
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Gaps
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                                          APPLICANT: Many Zhiwei
APPLICANT: Zhao, Qing A.
APPLICANT: Zhao, Qing A.
APPLICANT: Zhao, Qing A.
APPLICANT: Zhang, Jian-Rui
APPLICANT: Zhang, Jian-Rui
APPLICANT: Drmanac, Radoje T.
TITLE OF INVENTION: No. U820020150898A1e1 Nucleic Acids and
TITLE OF INVENTION: No. U820020150898A1e1 Nucleic Acids and
TITLE OF INVENTION: Polypeptides
FILE REFERENCE: 791CIP2E
CURRENT APPLICATION NUMBER: 09/770,160
PRIOR FILING DATE: 2001-01-22
PRIOR FILING DATE: 2001-01-26
PRIOR APPLICATION NUMBER: 09/552,929
PRIOR FILING DATE: 2000-04-18
NUMBER OF SEQ ID NOS: 18
SOFTWARE: PL-genes Version 2.0
CON TH. NO.
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TITLE OF INVENTION: No. US20020150898Alel Nucleic Acids and
TITLE OF INVENTION: Polypeptides
TITLE OF INVENTION: Polypeptides
TITLE OF INVENTION: Polypeptides
TITLE REFERENCE: 791C1P2E
CURRENT FILLNG DATE: 2001-03-22
CURRENT FILLNG DATE: 2001-03-22
PRIOR APPLICATION NUMBER: 09/770,160
PRIOR APPLICATION NUMBER: 09/770,160
PRIOR APPLICATION NUMBER: 09/552,929
PRIOR PILLNG DATE: 2000-04-18
NUMBER OF SEQ ID NOS: 18
SOFTWARE: PL-FL-genes Version 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 71.4%; Score 30; DB 10; Length 2260; Best Local Similarity 86.8%; Pred. No. 0.0093; Matches 33; Conservative 0; Mismatches 5; Indels (
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Patent No. US20020150898A1
GENERAL INFORMATION:
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Xue, Aidong J.
Ma, Yunging
Wang, Zhiwei
Zhao, Qing A.
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Zhang, Jie
Wang, Jian-Rui
Xue, Aidong J.
Ma, Yunqing
Wang, Zhiwei
Zhao, Qing A.
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APPLICANT: Zhou, Ping
APPLICANT: Goodrich, Ryle
APPLICANT: Asundi, Vinod
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; LOCATION: (1612)..(2142)
US-09-816-828-8
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| NAME/KEY: CDS
| LOCATION: (1612)..(2211)
| US-09-816-828-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: DNA ORGANISM: Homo sapiens
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ORGANISM: Homo sapiens
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US-09-816-828-9/c
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ch 71.4%; Score 30; DB 10; Length 2329; 1. Similarity 86.8%; Pred. No. 0.0094; 33; Conservative 0; Mismatches 5; Indels
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Pred. No. 0.6;
                                                                                                                                                                                                                                                                  Sequence 9, Application US/09765111A
Patent No. US20020106796A1
Patent No. US20020106796A1
Patent No. US20020106796A1
PAPLICANT: Fletcher, Jonathan A.
APPLICANT: Kroll, Todd G.
TITLE OF INVENTION: PAX8-PPRRgamma NUCLEIC ACID MOLECULES
TITLE OF INVENTION: ADD POLYPEPTIDES AND USES THEREOF
PILE REFERENCE: B0801/7196/ERP/MAT
CURRENT APPLICATION NUMBER: US/09/765,111A
CURRENT FILING DATE: 2001-01-18
PRIOR APPLICATION NUMBER: US 60/177,109
PRIOR FILING DATE: 2000-01-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Fletcher, Jonathan A.
APPLICANT: Fletcher, Jonathan A.
APPLICANT: Fletcher, Jonathan A.
APPLICANT: Fletcher, Jonathan A.
TITLE OF INVENTION: PANS-PPRRgamma NUCLEIC ACID MOLECULES
TITLE OF INVENTION: AND POLYPEPTIDES AND USES THEREOF
FILE REFERENCE: B0801/7196/ERP/MAT
CURRENT APPLICATION NUMBER: US/09/765,111A
CURRENT APPLICATION NUMBER: US 60/177,109
PRIOR FILING DATE: 2000-01-20
PRIOR APPLICATION NUMBER: US 60/177,109
PRIOR FILING DATE: 2000-01-14
NUMBER OF SEQ ID NOS: 47
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 3
LENGTH: 2523
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                                                                                                   5 CGCAGGCATGGTGGCAGAAATGACCATGGTTGACACAG 42
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION NUMBER: US 60/225,079
PRIOR FILING DATE: 2000-08-14
NUMBER OF SEQ ID NOS: 47
SCHTWARE: FASISEQ for Windows Version 3.0
SEQ ID NO 9
LENGTH: 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 3, Application US/09765111A Patent No. US20020106796A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 58.1%;
Best Local Similarity 82.4%;
Matches 28; Conservative
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ORGANISM: Homo Sapiens
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ORGANISM: Homo Sapiens
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; LOCATION: (1)...(2523)
US-09-765-111A-3
  Query Match
Best Local Similarity
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US-09-765-111A-9
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US-09-765-111A-9
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US-09-765-111A-3
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General information;
APPLICANT: TANABE SETYAKU CO. LTD.
APPLICANT: TANABE SETYAKU CO. LTD.
APPLICANT: TANIGUCHI, Tomoyasu
APPLICANT: MIZUKANI, Junko
TITLE OF INVENTION: METHOD FOR IDENTIFYING OR SCREENING AGONIST AND
TITLE OF INVENTION: ANTAGONIST TO PPAR
FILE REPERENCE: TANIGUCH:=6
CURRENT APPLICATION NUMBER: US/10/109,886
CURRENT FILING DATE: 2000-02-28
FRIOR FILING DATE: 2000-02-28
FRIOR FILING DATE: 1998-08-24
FRIOR FILING DATE: 1999-08-24
FRIOR FILING DATE: 1997-08-27
NUMBER OF SEQ ID NOSE: 10
SOFTWARE: Patentin version 3.0
SOFTWARE: Patentin version 3.0
                                                          Gaps
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Pred. No. 1.7;
0; Mismatches 8; Indels 0;
         Length 2523;
                                                                                                                                                                                                                                                       Sequence 15, Application US/09765111A

Patent No. US20020106796A1

GENERAL INFORMATION:

APPLICANT: Fletcher, Jonathan A.

APPLICANT: Kroll, Todd G.

TITLE OF INVENTION: PAX8-PPRGamma NUCLEIC ACID MOLECULES

TITLE OF INVENTION: AND POLYPEPTIDES AND USES THEREOF

FILE REFERENCE: B0801/7196/ERRP/MAT

CURRENT FILING DATE: 2001-01-18

PRIOR APPLICATION NUMBER: US 60/177,109

PRIOR PILING DATE: 2000-01-20

PRIOR PILING DATE: 2000-01-20

PRIOR PILING DATE: 2000-01-20

PRIOR PILING DATE: 2000-08-14

NUMBER OF SOU ID NOS: 47

SOUTWARE PASSEQ for Windows Version 3.0
                                                        Indels
       Score 24.4; DB 10;
Pred. No. 1.5;
0; Mismatches 6;
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                                                                                                                                      Db 1075 GCCTCCTCTGAGAATGACCATGGTTGACACAG 1108
                                                                                               9 GGCATGGTGGCAGAAATGACCATGGTTGACACAG 42
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US-10-109-886-5
Sequence 5, Application US/10109886
; Patent No. US20020119499A1
  58.1%;
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Best Local Similarity 78.4%;
Matches 29; Conservative (
Query Match
Best Local Similarity 82.4%
Matches 28; Conservative
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; LOCATION: (91)...(1608)
US-09-765-111A-15
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NAME/KEY: CDS
LOCATION: (159)..(1679)
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ORGANISM: Homo Sapiens
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ORGANISM: Homo sapiens
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US-09-765-111A-15
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                                            Query Match 57.6%; Score 24.2; DB 12; Length 1679; Best Local Similarity 78.4%; Pred. No. 1.7; Matches 29; Conservative 0; Mismatches 8; Indels 0;
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                                                                                                                                                                                                                                                                                                                Sequence 37, Application US/09765111A
Patent No. US20020106796A1
GAPREAL INCRMATION:
APPLICANT: Fletcher, Jonathan A.
APPLICANT: Fletcher, Jonathan A.
TITLE OF INVENTION: PAX8-PPRAgamma NUCLEIC ACID MOLECULES
TITLE OF INVENTION: PAX8-PPRAgamma NUCLEIC ACID MOLECULES
TITLE OF INVENTION: PAX8-PPRAgamma NUCLEIC ACID MOLECULES
TITLE OF INVENTION: AND POLYPEPTIDES AND USES THEREOF
E REFERENCE B0801/7196/REP/NAT
CURRENT FILING DATE: 2001-01-18
PRIOR FILING DATE: 2000-01-20
PRIOR FILING DATE: 2000-01-20
PRIOR FILING DATE: 2000-08-14
NUMBER OF SEQ ID NOS: 47
SOSTWARE: FastSEQ for Windows Version 3.0
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C. -765-111A-36

D. C. -765-111A-36

Sequence 36, Application US/09765111A

Patent NO. US20020106796A1

SENERAL INFORMATION:
APPLICANT: Fletcher. Jonathan A.
APPLICANT: Fletcher. Jonathan A.
APPLICANT: Fletcher. Jonathan A.
TITLE OF INVENTION: PAX8-PPARgamma NUCLEIC ACID MOLECULES
FILE REPRENCE: B0801/1956/ERP/MAT
CURRENT APPLICATION NUMBER: US/09/765,111A

CURRENT APPLICATION NUMBER: US/09/765,111A

PRIOR PLING DATE: 2000-01-20
PRIOR FLING DATE: 2000-01-20

PRIOR FLING DATE: 2000-01-20

PRIOR FLING DATE: 2000-01-20

PRIOR FLING DATE: 2000-01-20

SEQ ID NO3: 47

SEQ ID NO 36

LENGTH: 537

LENGTH: 537
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; OTHER INFORMATION: n = A or T or C or G or other
US-09-765-111A-37
                                                                                                                                                                              225 GCAAACATATCACAAAAAGAAATGACCATGGTTGACACAG 261
                                                                                                                                                 6 GCAGGCATGGTGGCAGAAATGACCATGGTTGACACAG 42
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Best Local Similarity 95.8
Matches 23, Conservative
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ORGANISM: Homo Sapiens
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ORGANISM: Homo Sapiens
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NAME/KEY: Unknown
LOCATION: (85)...(85)
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US-09-765-111A-37
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LENGTH: 348
US-10-109-886-5
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; OTHER INFORMATION: n = A or T or C or G or other US-09-765-111A-36
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Query Match 53.3%; Score 22.4; DB 10; Length 537; Best Local Similarity 95.8%; Pred. No. 6.6; Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps
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 1 CCATCGCAGGCATGGTGGCAGAAA 24

 Db
 356

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Search completed: January 22, 2003, 02:10:00 Job time : 29 secs

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AA161363 2q39b10.s
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AA53686 aa18908.r
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A1375926 tc14d11.x
A1777396 EST263804
BF032197 601452611
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BH110027 RPCI-24-3
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BI535582 399198 MA
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BE294158 601172919
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                                                                            601681083
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BE899540 601681793
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Bukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.
1 (Dases 1 to 903)
Lil, W.B., Gruber, C., Jessee, J. and Polayes, D.
Full-length CDNA libraries and normalization
Unpublished (2001)
                                                                                                   AL826215 AL826215
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BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ALIGNMENTS
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AW653703
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BI535582
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AI777396
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TITLE
JOURNAL
COMMENT
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ALS43579
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KEYWORDS
SOURCE
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BM922116 AGENCOURT
BI820841 603034063
BM92448 AGENCOURT
AQ012491 CIT.HSP-2
BB619013 BB619013
                                                                         January 21, 2003, 23:02:45; Search time 1003.67 Seconds (without alignments) 677.725 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                             42
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                                                                                                                                             1 ccatcgcaggcatggtggca.....aatgaccatggttgacacag
                                                                                                                                                                                                                          32308132
         GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
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                                                                                                                                                                                                    16154066 segs, 8097743376 residues
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Maximum Match 100%
Listing first 45 summaries
                                                    - nucleic search, using sw model
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BM922116
BI820841
BM924484
AQ012491
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em_gss_inv: *
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Maximum DB seq length: 200000000
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30
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Perfect score:
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                                                      OM nucleic
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No.
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68 CGCCGCCGTGGCCGCAGAATGACCATGGTTGACACAG 105

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1. .901
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Best Local Similarity
Matches 29; Conserv
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                                                                                                                                   DEFINITION
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JOURNAL
COMMENT
                                                                                                                                                                                ACCESSION
                                                                      RESULT 3
BI820841
                                                                                                                                                                                                                                                                                                                                   REFERENCE
                                                                                                                                                                                                                                                                                                                                                        AUTHORS
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BM924484
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KEYWORDS
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enriched, double-stranded cDNA was digested with Not I and cloned into the Not I and Eco RV sites of the pcWNSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies. Contact: Feng Library was constructed by a division of Invitrogen 9800 Medical Center Drive Rockville, Maryland 2080, USA Fax: (1) 301 610 8371 http://fulllength.invitrogen.com"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="Organ: pooled brain, lung, testis; Vector:
pCMV-SPORT6; Site 1: Not!; Site 2: BcoRV (destroyed); RNA
source anonymous pool of 6 male brains, age range 23-27; 1
male lung, age 27; and 1 male testis, age 69. Library is
oligo-dT primed and directionally cloned (BcoRV site is
destroyed upon cloning). Average insert size 1:8 kb,
insert size range 1-3 kb. Library is normalized and
enriched for full-length clones and was constructed by C.
Gruber (Invitrogen). Research Genetics tracking code
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1 (bases 1t o 1141)
NIH-MGC http://mgc.nci.nih.gov/.
NIH-MGC http://mgc.nci.nih.gov/.
Unational Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
plate: LLAMI2791 row: d column: 12
High quality sequence stop: 105.
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                                                                                                                                                                                                                                             9; Length 903;
                                                                                                                                                                              1 others
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021. Note: this is a NIH_MGC Library."
a 291 c 301 g 259 t 2 othe
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                                                                                                                                                                                                                                                                                                                                                     96 CGCCGCCGTGGCCGCAGAATGACCATGGTTGACACAG 133
                                                                                                                                                                                                                                                                                                                             5 CGCAGGCATGGTGGCAGAAATGACCATGGTTGACACAG 42
                                                                                                                                                                                                                                      Score 30; DB 9;
Pred. No. 0.75;
0; Mismatches
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Pred. No. 0.83;
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/db.xref="taxon:8606"
/clone="IMAGE:5754203"
/clone=lib="NHH MGC_115"
/lab_host="DH10B"
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86.8%;
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86.8%;
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                                                                                                                                                                                                                                                                                    33; Conservative
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Best Local Similarity
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Best Local Similarity
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AUTHORS
TITLE
JOURNAL
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BM922116
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Gaps

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5; Indels

0; Mismatches

33; Conservative

Matches

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5 CGCAGGCATGGTGGCAGAATGACCATGGTTGACACAG 42

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/lab.host="Organ: pooled brain, lung, testis; Vector:
pCWN-spoore; Site_1: bocis, Site_2: Bocok (destroyed); RNA
source anonymous pool of 6 male brains, age range 23-27;
male lung, age 27; and 1 male testis, age 69. Library is
oligo-dr primed and directionally Choned (Bocoky site is
destroyed upon cloning). Average insert size 1.8 kb,
insert size range 1-3 kb. Library is normalized and
enriched for fill-length clones and was constructed by C.
Gruber (Invitrogen). Research Genetics tracking code
021. Note: this is a NIH MGC Library."
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EST 04-OCT-2001
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                                                                                                                                                                                                                                                                                                                                                                                                Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/Libra at:
http://image.llnl.gov
Plate: LLAMI1436 row: m column: 16
High quality sequence stop: 876.
Location/Qualifiers
                  603034063F1 NIH_MGC_115 Homo sapiens cDNA clone IMAGE:5175351 5',
                                                                                                                                                                                                                             Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 901)
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Mammalia; Butheria, Primates, Catarrhini, Hominidae, Homo.
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National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
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linear
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/clone_lib="NIH_MGC_115"
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301 bp
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NIH-MGC http://mgc.nci.nih.gov/.
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1 Similarity 78.4%;
29; Conservative (
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Gaps

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Fax: 81-45-503-9216

Fax: 81-45-503-9216

Email: genome-res@gsc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp,
Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh
,M., Konho,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new
genes. Genome Res. . 10 (10), 1617-1630 (2000)
wagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E.,
Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,U., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and
Hayashizaki,Y.
RIKEN integrated sequence analysis (RISA) system-.384-format
sequencing pipeline with 384 multicapillary sequencer. Genome Res.
10 (11), 1757-1771 (2000)
Konno,H., Fukunishi,Y., Shibata,K., Itoh,M., Carninci,P., Sugahara
,Y. and Hayashizaki,Y.
Computer-based methods for the mouse full-length cDNA
encyclopedia: real-time sequence clustering for construction of a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 62).

Arakawa, T., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hiramoto, K., Hori, F., Ishii, Y., Ito, M., Kawai, J., Konno, H., Kouda, S., Matsuyama, T., Miyazaki, A., Nomura, K., Ohno, M., Chazaki, Y., Okido, T., Saaraki, A., Nomura, K., Ohno, M., Tagawa, A., Shiraki, T., Sakai, K., Sano, H., Sasaki, D., Shibata, K., Shinaka, A., Shiraki, T., Sogabe, Y., Suuki, H., Muramatsu, M., Tagawa, A., Takahashi, F., Takeda, Y., Tanaka, T., Toya, T., RIKEN Mouse Este (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BB619013 RIKEN full-length enriched, 8 days embryo Mus musculus CDNA clone 5730466120 5', mRNA sequence.
           http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html.
Seg primer: M13-21
Class: BAC ends.
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Tel: 81-45-503-9222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: Yoshihide Hayashizaki
Laboxatory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(SGS), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
                                                                                                                                                                                                                                                                                                                /cell_type="Sperm"
/note="Vector: pBeloBAC11; Site_1: HindIII; Site_2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 426;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
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Pred. No. 1.4e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                         101
                                                                                                                                                                            db_xref="GDB:7154711"
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clone="2300P19"
clone lib="CIT-HSP"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           629 bp
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76.3%;
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="Organ: pooled colon, kidney, stomach, Vector:
    pCMV-SPORT6; Site_1: Not1; Site_2: EccRV (destroyed); RNA
    source anonymous pool of 3 colons, age 26 yo male, 49 yo
    female, 71 yo male colon; 46 yo male kidney, and pool of 2
    stomachs, 62 yo male and 70 yo female. Library is
    oligo-dT primed and directionally cloned (EccRV site is
    destroyed upon cloning). Average insert size 1.4 kb,
    insert size range 1.3 kb. Library is normalized and
    enriched for full-length clones and was constructed by C.
    druber. Invitrogen). Research Genetics tracking code
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Adams, M.D., Rounsley, S.D., Zhao, S., Field, C.E., Bass, S., Linher, K., Golden, K., Berry, K., Granger, D., Suh, E., Wible, C., Shizuya, H., Simon, M., and Venter, Y. Granger, D., Suh, E., Wible, C., Shizuya, H., Use of a random BAC End Sequence Database for Sequence-Ready Map Building (1998)
Unpublished (1998)
Other GSSs. CIT-HSP-2300P19.TR
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
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Clones are availabe from Research Genetics (info@resgen.com). BAC
end search page:
                                                                                                                                                                                       DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://fmage.llnl.gov
Plate: LLAM12808 row: i column: 01
High quality sequence start: 95
High quality sequence start: 95
Location/Qualifiers
National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)
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                                                   Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Fax: 301 838 0208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          023. Note: this is a NIH MGC Library."
                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /clone_lib="NIH_MGC_116"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /db_xref="taxon:9606"
/clone="IMAGE:5760840"
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AQ012491.1 GI:3185056
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Yamanaka,I., Kiyosawa,H., Kondo,S., Saito,T., Shinagawa,A., Aizawa
,X., Fukuda,S., Hara,A., Itoh,M., Kawai,J., Shibata,K., Arakawa,T., Ishii,Y. and Hayashizaki,Y.
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Pan troglodytes DNA, clone: RP43-058C03.TJ, genomic survey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="Site 1: Sal1; Site 2: BamH1; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. 1st strand cDNA was
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pan troglodytes male lymphocytes DNA, clone_lib:RPCI-43 Chimpanzee Male BAC Library clone:RP43-058C03.TJ.
Pan troglodytes
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Pan.
                                                                                                                                                                                                                                                                                                                                                                     /clone_lib="RIKEN full-length enriched, 8 days embryo"
/sex="mixed"
                                                                                                Mapping of 19032 mouse cDNAs on mouse chromosomes. J. Struct. Fruc. Genomics 2 pre, L72-L86 (2001 Please visit our web site (http://genome.gsc.riken.go.jp) for further details.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Fujiyama, A., Hattori, M., Toyoda, A., Taylor, T.D., Yada, T., Totoki, Y., Watanabe, H. and Sakaki, Y. Gerd sequences of Library RPCI-43 Unpublished
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                                                                                                                                                                                                                                                                                                                                                                                                                   /dev_stage="8 days embryo"
/lab_host="DH108"
                                                                                                                                                                                                                                                                          organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                     /db_xref="taxon:10090"
/clone="5730466120"
                                                                                                                                                                                                                       Location/Qualifiers
                                                                                                                                                                                                                                                                                                   /strain="C57BL/6J'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AG184368
AG184368.1 GI:16714048
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(E-mail:chimpbes@gsc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/, Tel:81-45-503-9111, Fax:81-45-503-9170)
Clones are derived from the chimpanzee BAC library RPCI-43 This BAC end was generated during the RkD process and may have higher chance
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EST 12-MAR-1998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2q39bl0.sl Stratagene hNT neuron (#937233) Homo sapiens cDNA clone NANF 522059 3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

[bases 1 to 318]
Hillier, L., Allen, M., Bowles, L., Dubuque, T., Geisel, G., Jost, S., Krizman, D., Kucaba, T., Lacy, M., Le, N., Lennon, G., Marra, M., Martin, J., Moore, B., Schellenberg, K., Steptoe, M., Tan, F., Theising, B., Washb-NcI human Est Project
Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /clone_lib."Stratagene hNT neuron (#937233)"
/clone_lib."Stratagene hNT neuron (#937233)"
/dev_stage="hNT neurons"
/lab_host="SOLM (kanamycin resistant)"
/note="Yector: pBluescript SK-; Site_1: BcoRI; Site_2:
XhoI; Cloned unidirectionally. Primer: Oligo dT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Possible reversed clone: polyT not found Insert Length: 1847 Std Error: 0.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                /sex="male"
/cell_type="lymphocytes"
/clone_lib="RPCI-43 Chimpanzee Male BAC Library"
1 447 c 220 g 545 t 94 others
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
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Washington University School of Medicine
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High quality sequence stop: 257.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                          /organism="Pan troglodytes"
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/db_xref="GDB:5182140"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                               /db_xref="taxon:9598"
/clone="RP43-058C03.TJ"
                                                                                                                                                                                                                                                  te 2 : EcoRI.
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                                                                                                                                                                                                 Vector : pBACe3.6
R.Site 1 : EcoRI
R.Site 2 : ECORI.
                                                                                                 of clone tracking errors.
PRIMERS
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AA161363.1 GI:1735599
                                                                                                                                                     Sequencing: TJ
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EST 25-SEP-2001

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RESULT 9 AQ614173 NOI

Ad 31C VERSION

ORGANISM

KEYWORDS

SOURCE

REFERENCE AUTHORS

MEDLINE COMMENT

JOURNAL

TITLE

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1 (bases 1 to 451)
McCarter,J., Clifton,S., Chiapelli,B., Pape,D., Martin,J., Wylie,T.,
Dante,M., Marra,M., Hillier,L., Kucaba,T., Theising,B., Bowers,Y.
Gibbons,M., Ritter,E., Bennett,J., Franklin,C., Tsagareishvili,R., Ronko,I., Kennedt,S., Maguire,L., Beck,C., Underwood,K., Steptoe,M., Allen,M., Person,B., Swaller,T., Harvey,N., Schurk,R., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R., Waterston,R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PCR based library using a modified protocol from the SWART PCR cDNA Synthesis Kit from Clontech. Directionally cloned into the UDG sites of pAMPI. Nematocloses are the OP50 strain developed by Dr. Charlie Opperman of North
                                                                                                                                                                                                                                                                                                                                                                                           Heterodera glycines
Bukaryota, Metazoa, Nematoda, Chromadorea, Tylenchida, Tylenchina,
Tylenchoidea, Heteroderidae, Heteroderinae, Heterodera.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="Vector: pAMP1 (Gibco); Site 1: Not1, Site 2: Sal1; The library was constructed by Brandi Chiapelli and Dr. James McCarter at Washington University, St. Louis. The CDNA was made by using Dynabead oligo-dT priming (Dynal).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The library was constructed by Brandi Chiapelli and Dr. James McCarter (bchiapel@watson.wustl.edu & jmccarte@watson.wustl.edu) Washington University Garome Sequencing Center St. Louis. Washington University Garome Sequencing Center St. Louis. High quality sequence stop: 399.
                                                                                                                                                        ro65e07.yl Heterodera glycines J2 pAMP1 v8 Chiapelli McCarter Heterodera glycines J2 pAMP1 v8 Chiapelli McCarter repetitive element ;, mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Heterodera glycines"
/db_xref="taxon:51029"
/clone_lib="Heterodera glycines J2 pAMP1 v8 Chiapelli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Unpublished (1999)
Contact: McCarter Up
The Washington Univ. Nematode EST Project, 1999
Washington Univ. School of Medicine
Mashington University School of Medicine
TH44 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1810
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/lab_host="DH10B"
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26 CCATTCCAGGCATNGCGACCAAAAATACCATGGTTNANA 64
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HS 5127_B2 F07 T7A RPCI-11 Human Male BAC Library Homo saplens enomic_clone Flate=703 Col=14 Row=L, DNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="Vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI;
Male blood DNA was isolated from one randomly chosen donor and partially digested with a combination of EcoRI and EcoRI Methylasse. Size selected DNA was cloned into the pBACe3.6 vector at EcoRI sites"

124 c 115 g 152 t 11 others
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Fax: (206) 616-3887

Email: jwallace@u.washington.edu
Clones are derived from the human BAC library RPCI-11. For BAC
library availability, please contact Pieter de Jong
(pieter@dejong.med.buffalo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/ordering_bac.htm)
or from Resear h Genetics (info@resgen.com). BAC end Web Server:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence-tagged connectors: A sequence approach to mapping and scanning the human genome Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)
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                                                                                                                                                                                        55.7%; Score 23.4; DB 9; Length 318; 73.2%; Pred. No. 1.5e+02; ive 0; Mismatches 11; Indels
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University of Washington
401 Queen Anne Avenue North, Seattle, WA 98109, USA
Tel: (206) 616-3618
                                                                                                             2 others
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High quality sequence stop: 594.
Location/Qualifiers
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Seg primer: T7
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Mahairas, G.G., Walla
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at

0 EST 06-JUN-2000 Gaps ; 0 Score 23; DB 13; Length 451; Pred. No. 2.4e+02; 0; Mismatches 10; Indels linear 251 ArcGGCGGAArGGCGGCAGAArGCACATTTCGACTCA 289 3 ATCGCAGGCATGGTGGCAGAATGACCATGGTTGACACA 41 mRNA 122 t dq 009 BE019930 RESULT 11 BE019930 LOCUS

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Query Match

Matches

BASE COUNT

FEATURES

146:1311-8, 1997

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Homo sapiens
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| / Lab host="DH10B (phage=resistant)" |
| / Lab host="DH10B (phage=resistant)" |
| / Lab host="DH10B (phage=resistant)" |
| / Lab host="DH10B (phage=resistant)" |
| / Local corned no vary, vector porps; site_l: XhoI; site_2:
| ECORI, CDNA made by oligo-dT priming. Directionally |
| Cloned into EcoRI/XhoI sites using the following 5' |
| adaptor: GGCAGGAG(0). Size=selecced >500bp for average |
| insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit |
| (Stratagene) and Supersoript II RT (Life Technologies)."
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                                                                                                                                                                                                                                                                                                                                                         Email: cgapbs-r@mail.nih.gov
Tissue Procurement: DCTD/DTP
CDN Library Preparation: Ling Hong/Rubin Laboratory
CDN Library Preparation: Ling Hong/Rubin Laboratory
CDN Library Arrayed by: The I.M.A.G.E. Consortium (LLML)
DNA Sequencing by: Mashington University Genome Sequencing Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/Lubin at:
image.llnl.gov/image/html/lresources.shtml
Seq primer: -dopRP from Gibco
High quality sequence stop: 337.
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.

    (bases 1 to 600)

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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
bb62d12.v1 NIH MGC 9 Homo sapiens cDNA clone IMAGE:3030071 5' similar to gb:X696\overline{9}9 PAIRED BOX PROTEIN PAX-8 (HUMAN); gb:X57487 M.musculus mRNA Pax8 (MOUSE);, mRNA sequence.
                                                                                                                                                                                                                                                          NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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ilarity 74.4%; Pred. No. 2.7e+02;
Conservative 0; Mismatches 10
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/clone="IMAGE:3030071"
/clone_lib="NIH_MGC_9"
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                                                                                                                                                                                                                                                                                                                                        Contact: Robert Strausberg, Ph.D.
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Tissue Procurement: DCTD/DTP
                                                                                               BE019930.1 GI:8280021
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/Organization Jones Approx. / Organization Jone="LimAGE:3030422" / Clone="LimAGE:3030422" / Clone="LimAGE:3030422" / Clone lib="WAHH MGC 9" / Lissue_type="adenocarcinoma cell line" / Lissue_type="adenocarcinoma cell line" / Lissue_type="adenocarcinoma cell line" / Lissue_type="adenocarcinoma cell line" / Lissue="bong: Dana made by oligo-dar priming. Directionally cloned into Ecosil/Khol sites using the following 5' adaptor: GGCACGAG(G). Size-selected > Sidobp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZBA-CDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."
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0
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cDNA Library Preparation: Ling Hong/Rubin Laboratory CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Washington University Genome Sequencing Center Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov/image/html/iresources.shtml Seq primer: -40RP from Gibco High quality sequence stop: 508.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 (bases 1 to 612)
Dias Neto.B., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
Nagai.M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,
Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare
M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
Simpson,A.J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   QV1-HB0037-300101-591-e07 HB0037 Homo sapiens cDNA, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: Simpson A.J.G.
Labbzatory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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74.4%; Pred. No. 2.8e+02;
tive 0; Mismatches 10;
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                                                                                                                                                                                                                                                                                                                                                        /organism="Homo sapiens"
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High quality sequence stop: 631.
Location/Qualifiers
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Email: asimpson@ludwig.org.br
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20202663
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Best Local Similarity 74.1%
Matches 29, Conservative
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DEFINITION
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ORIGIN
                                                                                                                RESULT 15
AZ049319
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JOURNAL
MEDLINE
COMMENT
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KEYWORDS
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| lab host="DH10B (phage-resistant)"
| lub host="DH10B (phage-resistant)"
| luot="lorgan: ovary, vector: pOTB7; site_1: XhoI; Site_2:
| ROORI; cDNA made by oligo-dT priming. Directionally
| cloned into EcoRI/XhoI sites using the following 5'
| adaptor: GGCACGAG(G): Size-selected >500bp for average
| nnsert size 1.8kb. Library constructed by Ling Hong in
| the laboratory of Gerald M. Rubin (University of
| california, Berkeley) using ZAP-cDNA synthesis kit
| (Stratagene) and Superscript II RT (Life Technologies)."
           /Organism="Homo sapiens"
/db xref="taxon:9606"
/db xref="Homo:370"
/dous lib="Homo:370"
/dou'stage="Adult"
/note="Organ: bocio tumor; Vector: pucl8; Site_1: SmaI;
Site_2: SmaI; A mini-library was made by cloning products
derived from ORESTES POR (U.S. Letters Patent application
No. 196; 116 - Ludwig Institute for Cancer Research)
profiles into the pUC 18 vector. Reverse transcription of
tissue mRNA and coNA amplification were performed under
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BE898291 601681083F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3951356 5',
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S NIH-MGC http://mgc.nci.nih.gov/.

NIH-MGC http://mgc.nci.nih.gov/.

I Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbe: r@mail.nih.gov

Tissue Procurement: DCTD/DTP

CDNA Library Preparation: Ling Hong/Rubin Laboratory

CDNA Library Preparation: Ling Hong/Rubin Laboratory

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLML)

DNA Sequencing by: Incyte Genemics, Inc.

Clone distribution: MGC Clone distribution an be
found through the I.M.A.G.E. Consortium/LLML at: image.llnl.gov
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Mammalia; Eutheria, Primates, Catarrhini, Hominidae, Homo.
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                                                                                                                                                                                                                                                                                                                                              Length 632;
                                                                                                                                                                                                                                                                      1 others
                                                                                                                                                                                                                                                                                                                                                                                    10; Indels
                                                                                                                                                                                                                                                                                                                                         Score 23; DB 13;
Pred. No. 2.8e+02;
0; Mismatches 10;
                                                                                                                                                                                                                                                                                                                                                                                                                               1 CCATCGCAGGCATGGTGGCAGAAATGACCATGGTTGACA 39
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                                                                                                                                                                                                                                                   low stringency conditions."
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Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /db_xref="taxon:9606"
/clone="IMAGE:3951356"
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                                                                                                                                                                                                                                                                                                                                       54.8%;
ilarity 74.4%;
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Best Local Similarity
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DEFINITION
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BE898291
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AUTHORS
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AZ049319 511 bp DNA linear GSS 06-MAR-2001
GSSBru0872 Sheared genomic library Brucella melitensįs biovar
Abortus genomic clone Bc09, DNA sequence.
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Instituto Nacional de Tecnologia Agropecuaria (INTA) C.C. 25 (1712)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (STRATAGENE); Genomic DNA
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Sanchez, D.O., Zandomeni, R.O., Cravero, S., Verdun, R.E., Pierrou, E.,
Sanchez, D. Daz, G. Lanzavecchia, S., Aguero, F., Frasch, A.C.C.,
Andersson, S.G.E., Rosetti, O.L., Grau, O. and Ugalde, R.A.
Gene discovery through genomic sequencing of Brucella abortus
Infect. Immun. 69 (2), 865-868 (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /Glone lib="Gheared genomic library"
/Glone lib="Obctor: pBluescript SK(-) (STRATAGENE); Genomic DN
was mechanically sheared, blunt ended, and
size-fractionated by agarose gel electrophoresis.
Fragments between 1.5-3 KD were recovered and ligated to
the EcoRV site of the pBluescript SK (-) vector."
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Brucella melitensis biovar Abortus
Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
Brucellaceae; Brucella.
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                                  113 CCATGGCAGGCATGGTGGCAGGTAAGGAGGGCGGCA 151
CCATCGCAGGCATGGTGGCAGAAATGACCATGGTTGACA 39
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Tel: 5411-4621-3316/1683
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/clone="Bc09"
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Location/Qualifiers
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Best Local Similarity 79.49
Matches 27, Conservative
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Gaps

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54.8%; Score 23; DB 12; Length 637; 74.4%; Pred. No. 2.8e+02;

0; Mismatches 10; Indels

Conservative

1 Similarity 29; Conserv

Best Loca Matches

Query Match Local